

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
19 73 42.88

Times: CPU Total Elapsed
00:01:14.89 00:03:25.00

Number of residues: 1211939
Number of sequences optimized: 3953

The scores below are sorted by optimized score.
Significance is calculated based on optimized score.

3 100% identical sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. P80713	Complete sequence of the matu	295	295	295	6.44	0
2. P80504	Sequence encoded by human tis	295	295	295	6.44	0
3. P81503	Human tissue factor	295	295	295	6.44	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
4. P93986	**** 6 standard deviations above mean **** Human tissue factor apoprotei	295	293	293	6.39	0
5. R28067	**** 5 standard deviations above mean **** Sequence encoded by truncated	251	251	251	5.41	0
6. R39392	**** 4 standard deviations above mean **** Truncated tissue factor.	218	217	217	4.62	0
7. R07072	Human tissue factor activator	209	177	207	4.38	0
8. R10065	**** 3 standard deviations above mean **** Newcastle disease virus (NDV)	553	7	157	3.22	0
9. R14480	Newcastle disease virus immun	553	7	156	3.19	0
10. R22217	Sequence of interleukin 5 rec	415	6	155	3.17	0
11. R22211	Sequence of interleukin 5 (IL	415	6	155	3.17	0
12. R22212	Sequence of interleukin 5 (IL	398	6	155	3.17	0
13. P70176	Sequence of Newcastle Disease	553	7	155	3.17	0
14. R08031	Adenyl cyclase from Bordetell	1706	7	154	3.15	0
15. R05041	Filamentous haemagglutinin A.	3647	6	154	3.15	0
16. R12108	N-terminal deleted adenyl cyc	1445	7	154	3.15	0
17. P93357	Sequence of the catalytic dom	1522	7	154	3.15	0
18. P94365	Sequence of part of adenylate	1705	7	154	3.15	0
19. R04716	Amino acid sequence of the 65	572	6	153	3.12	0
20. R04713	Amino acid sequence of the hu	573	8	153	3.12	0
21. P80215	Sequence of Mycobacterium tub	560	6	153	3.12	0
22. R04715	Amino acid sequence of the 65	573	6	153	3.12	0
23. R27481	RP-III residual protease.	806	6	153	3.12	0
24. R27745	Extracellular factor related	1822	6	153	3.12	0
25. P80364	M. leprae 65kD antigen.	588	6	152	3.10	0
26. R06376	Product of the sscI gene.	950	7	152	3.10	0
27. R05701	Human carbastatin polypeptide	673	7	152	3.10	0
28. P70768	Epstein-Barr virus glycoprote	927	7	152	3.10	0
29. P82115	Fibronectin binding protein.	1018	6	152	3.10	0
30. R13251	PECAM-1.	738	7	152	3.10	0
31. R22220	Sequence of secretory interle	396	6	151	3.08	0
32. R10941	Mutant protease (delta137-139	1968	10	151	3.08	0
33. R11137	GAP6 encoded by lambda clone	1047	7	151	3.08	0
34. R13335	HypB protein.	544	6	151	3.08	0
35. R25336	Lambda clone 101 protien.	1047	7	151	3.08	0
36. R33181	L3T4 mutant M8.	454	7	151	3.08	0
37. R12789	M. pneumoniae P1 cytoadhesin p	1627	6	151	3.08	0
38. R06723	Achromobacter protease I.	653	6	151	3.08	0
39. P60723	Sequence of extracellular amy	918	6	151	3.08	0
40. R22219	Sequence of secretory interle	420	6	151	3.08	0

1. FURM-969863-FIG2.PEP (1-295)
P80713 Complete sequence of the mature and precursor form

ID P80713 standard; peptide; 295 AA.
AC P80713;
DT 10-SEP-1990 (first entry)
DE Complete sequence of the mature and precursor forms of human tissue
DE factor heavy chain proteins (huTFh and pre-huTFh, respectively)
KW Human tissue factor heavy chain (huTFh); immunoassays;
KW precursor human tissue factor heavy chain (pre-huTFh);
KW human tissue factor detection.
OS Homo sapiens.
FH Key Location/Qualifiers
CT Peptide 1 72

FT Protein 33..33
 FT Region 33..62
 FT /note="claimed in claim 26.4"
 FT Region 58..80
 FT /note="claimed in claim 26.1"
 FT Region 62..103
 FT /note="claimed in claim 22"
 FT Region 73..81
 FT /note="claimed in claim 26.6"
 FT Region 88..103
 FT /note="claimed in claim 26.7"
 FT Region 126..155
 FT /note="claimed in claim 26.9"
 FT Region 178..199
 FT /note="claimed in claim 26.2"
 FT Region 187..199
 FT /note="claimed in claim 23"
 FT Region 193..222
 FT /note="claimed in claim 26.3"
 FT Region 222..241
 FT /note="claimed in claim 26.1"
 PN WD8807543-A.
 PD 06-OCT-1988.
 PF 29-MAR-1988; U00998.
 PR 25-JUN-1987; US-067103.
 PA (SCRI-) Scripps Clinic Res.
 PI Eddington TS, Morrissey JH;
 DR WPI; 88-292837/41.
 DR N-PSDB; N80743.
 PT New DNA segment -
 PT has gene encoding human tissue factor heavy chain protein and is
 PT useful for inhibiting coagulation
 PS Disclosure; Fig 1 and Fig 2; 148pp; English.
 CC It is the amino acid residue sequence of the predominant naturally
 CC occurring mature protein form residues 33 to 295. The sequence of the
 CC lesser found mature form begins at amino acid residue number 35 and ends
 CC at residue 295. A DNA segment which codes for it from about residue 33
 CC to 295 is claimed in claim 2. Also claimed are antibodies which
 CC immunoreact with huTFH and the claimed peptides (see FT). The antibodies
 CC may be used in immunoassays for detection of huTFH. The claimed peptides
 CC may be used to inhibit the binding of huTF to coagulation factor VII/VIIa
 CC in vivo. The claimed peptides have an N-terminal H and a C-terminal OH.
 SQ Sequence 295 AA;
 SQ 16 A; 12 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;
 SQ 15 I; 20 L; 20 K; 2 M; 13 F; 14 P; 23 S; 30 T; 7 W; 12 Y; 30 V;

Initial Score = 295 Optimized Score = 295 Significance = 6.44
 Residue Identity = 100% Matches = 295 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

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X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNGVYTVQIST
|||||
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNGVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLTYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLTYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSHKCRKAGVGQSWKE
      220     230     240     250     260     270     280

290   X
      NSPLNVS
      |||||
      NSPLNVS
290   X
  
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2. FURM-969863-FIG2.PEP (1-295)
 P80504 Sequence encoded by human tissue factor protein (T

ID P80504 standard; protein; 295 AA.
 AC P80504;
 DT 19-NOV-1990 (first entry)
 DE Sequence encoded by human tissue factor protein (TF) clone derived from

DE adipose cDNA library
KW Hybridisation; coagulation; blood clotting; therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..32
FT Protein 33..295
PN EP-278776-A.
PD 17-AUG-1988.
PF 12-FEB-1988; 301190.
PR 7-APR-1987; US-035409..
PR 05-FEB-1988; US-152698.
PA (GETH) Genentech Inc.
PI Lawn RM, Wion KL, Vehar GA;
DR WPI; 88-229602/33.
DR N-PSDB; n81104.
PT Tissue factor protein and derivs. -
PT obtd. by recombinant deoxyribonucleic acid techniques, used to
PT treat chronic bleeding and coagulation-disorders
PS Claim 5; Fig 2a-2b; 39pp; English.
CC Tissue factor protein (TFP) free of substances from its natural source is
CC claimed. TFP is administered providing a coagulation inducing therapeutic
CC compsn. for various chronic bleeding disorders. Two oligo probes
CC representing one possible codon choice for each AA of the N-terminal AA
CC sequence (60 nucleotides) and internal AA sequence near the C-terminal
CC (81 nucleotides) were designed and synthesised. cDNA clones of human TFP
CC were obtd. using the DNA probes first to screen a human placental cDNA
CC library. 1400 BP EcoRI fragment from a placental clone was used to screen
CC a human adipose cDNA library. The full length human TFP cDNA was contd.
CC within the cDNA clone lambda TF14. The full length cDNA was inserted into
CC an expression plasmid and TFP was expressed using mammalian cells (COS)
CC cells and E.coli.
SQ Sequence 295 AA;
SQ 16 A; 12 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;
SQ 15 I; 20 L; 20 K; 2 M; 13 F; 14 P; 23 S; 30 T; 7 W; 12 Y; 30 V;

Initial Score = 295 Optimized Score = 295 Significance = 6.44
Residue Identity = 100% Matches = 295 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQIST
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGSWKE
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGSWKE
     220     230     240     250     260     270     280

290   X
NSPLNVS
|||||
NSPLNVS
290   X

```

3. FURM-969863-FIG2.PEP (1-295) P81503 Human tissue factor

ID P81503 standard; protein; 295 AA.
AC P81503;
DT 22-OCT-1990 (first entry)
DE Human tissue factor
KW human tissue factor (HTF) apoprotein; procoagulant;
KW Factor VIII; ss.
OS synthetic.
FH Key Location/Qualifiers
FT Domain 33..220
FT /label=extracellular domain
FT Domain 221..243
FT /label=membrane domain
FT Domain 244..263
FT /label=cytoplasmic domain
FT Peptide 1..32

FT /label=signal peptide
 PN W08809817-A.
 PD 15-DEC-1988.
 PF 08-JUN-1988; U01915.
 PR 2-JUN-1986; US-062166.
 PR 14-MAR-1988; US-167870.
 PA (MOUN-) Mount Sinai Sch Med, (UYVA-) Yale University,
 PA (UYNY-) City Univ New York, (MOUN) Mount Sinai Hosp Res Fdn.
 PI Menerson Y, Konigsberg W;
 DR WPI; 88-368631/51.
 PT New recombinant cloning vehicle expressing human tissue factor -
 PT encoding DNA sequences, transformed cells and pure apoprotein
 PT prods
 PS Disclosure; pp; English.
 CC A cloned 2147bp cDNA fragment isolated from human placental cDNA
 CC library encodes a single chain polypeptide preprotein 295 long.
 CC The signal sequence is post translationally cleaved to give a mature
 CC protein of 263 amino acids.
 CC HTF can be used for inhibiting binding of factor VIII to tissue
 CC factor.
 CC See also N81950-2.
 SQ Sequence 295 AA;
 SQ 16 A; 12 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;
 SQ 15 I; 20 L; 20 K; 2 M; 13 F; 14 P; 23 S; 30 T; 7 W; 12 Y; 30 V;

Initial Score = 295 Optimized Score = 295 Significance = 6.44
 Residue Identity = 100% Matches = 295 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
      220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X

```

4. FURM-969863-FIG2.PEP (1-295)
 P93986 Human tissue factor apoprotein.

ID P93986 standard; protein; 295 AA.
 AC P93986;
 DT 22-MAY-1990 (first entry)
 DE Human tissue factor apoprotein.
 KW Human tissue factor; coagulation system; anticoagulant; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Sig_peptide 1..32
 FT /label= 32 AA leader
 FT Domain 33..251
 FT /label= Extracellular domain
 FT Domain 252..274
 FT /label= Membrane domain
 FT Domain 275..295
 FT /label= Cytoplasmic domain
 PN EP-347262-A.
 PD 20-DEC-1989.
 PF 19-JUN-1989; 306176.
 PR 17-JUN-1988; US-208895.
 PA (UYVA-) Yale Univ, (UYNY-) City Univ New York.
 PI Nemerson Y, Konigsberg W;
 DR WPI; 89-372479/51.
 DR N-PSDB; N92782.
 PT Cloning and expression of human tissue factor - for the prodn. of
 PT diagnostic reagents, anticoagulant agents and for experimental studies

PS Disclosure; pp; English.
 CC The protein is human tissue factor, which may be cloned from plasmid or
 CC bacteriophage vectors to produce pure or truncated tissue factor, useful
 CC for diagnostic reagents, anticoagulant agents and experimental purposes.
 CC Extracellular domain can be removed and used as a soluble tissue factor
 CC for use as diagnostic reagents, anticoagulant agents and experimental
 CC studies.
 SQ Sequence 295 AA;
 SQ 15 A; 13 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;
 SQ 15 I; 20 L; 20 K; 2 M; 13 F; 15 P; 24 S; 29 T; 6 W; 12 Y; 30 V;

Initial Score = 293 Optimized Score = 293 Significance = 6.39
 Residue Identity = 98% Matches = 292 Mismatches = 3
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGLWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARRLLLGLWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280

290   X
NSPLNVS
|||||
NSPLNVS
290   X

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5. FURM-969863-FIG2.PEP (1-295)
 R28067 Sequence encoded by truncated tissue factor (tTF)

ID R28067 standard; Protein; 251 AA.
 AC R28067;
 DT 02-APR-1993 (first entry)
 DE Sequence encoded by truncated tissue factor (tTF) cDNA.
 KW Activated factor VII; factor VIIa; truncated tissue factor.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..32
 FT /label= leader
 PN W09218870-A.
 PD 29-OCT-1992.
 PF 09-APR-1992; U02898.
 PR 10-APR-1991; US-683682.
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 PI Morrissey JJ;
 DR WPI; 92-382277/46.
 DR N-PSDB; Q29716.
 PT Assay for factor VIIa utilising truncated tissue factor - used to
 PT monitor factor VIIa therapy in haemophiliac(s), to screen for
 PT elevated factor VIIa levels and assess risk of thrombosis
 PS Disclosure; Fig 1; 37pp; English.
 CC Starting with clone pCTF543 a TF1-219 deletion mutant was
 CC constructed that contained the coding sequence for the predicted
 CC leader peptide and extracellular domains, but lacked the predicted
 CC transmembrane and cytoplasmic domains. This version of the protein
 CC retains cofactor activity but fails to support conversion of
 CC factor VII to VIIa. The essential difference between truncated
 CC tissue factor and wild-type tissue factor is that truncated tissue
 CC factor is no longer tethered to the phospholipid membrane surface.
 SQ Sequence 251 AA;
 SQ 13 A; 11 R; 14 N; 11 D; 0 B; 4 C; 9 Q; 20 E; 0 Z; 14 G; 0 H;
 SQ 7 I; 16 L; 17 K; 2 M; 11 F; 13 P; 19 S; 30 T; 6 W; 11 Y; 23 V;

Initial Score = 251 Optimized Score = 251 Significance = 5.41
 Residue Identity = 100% Matches = 251 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGLWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST

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7. FURN-969863-FIG2.PEP (1-295)
R07072 Human tissue factor activator.

ID R07072 standard; protein; 209 AA.
AC R07072
DT 10-JAN-1991 (first entry)
DE Human tissue factor activator.
KW Tissue factor; renal disease; sandwich immunoassay.
OS Homo sapiens.
PN M09008956-A.
PD 07-AUG-1990.
PF 02-FEB-1990; J00127.
PR 02-FEB-1989; JP-02263.
PR 17-FEB-1989; JP-036228.
PR 18-APR-1989; JP-096458.
PR 04-DEC-1989; JP-314602.
PA (TEIJ) TEIJIN KK.
PI Koike Y, Sumi Y, Ichikawa Y;
DR WPI: 90-261027/34.
PT Human tissue factor activator detection in human urine - by
PT sandwich immunoassay, for diagnosis of renal disease
PS Disclosure; page 5; 54pp; Japanese.
CC This apoprotein of human tissue factor (thromboplastin) differs
CC from that of known serum tissue factor. Its presence in e.g.
CC urine samples is determined using a sandwich immunoassay with one
CC or more monoclonal antibodies (MAbs) to this sequence. One Ab is
CC immobilised and the other labelled with e.g. an enzyme. It is
CC useful in the diagnosis of renal diseases such as nephritis,
CC nephrosis and kidney stones. See also R07073.
SQ Sequence 209 AA;
SQ 7 A; 7 R; 14 N; 11 D; 0 B; 4 C; 7 Q; 15 E; 0 Z; 10 G; 0 H;
SQ 7 I; 13 L; 16 K; 1 M; 9 F; 9 P; 19 S; 27 T; 4 W; 10 Y; 19 V;

Initial Score = 177 Optimized Score = 207 Significance = 4.38
Residue Identity = 99% Matches = 209 Mismatches = 0
Gaps = 1 Conservative Substitutions = 0

```

      10      20      30 X      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
      X      10      20      30      40
      SGTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST

      80      90      100      110      120      130      140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      50      60      70      80      90      100      110

      150      160      170      180      190      200      210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYKSSSSGKKTAKTNTNEFLIDVDKGEN
      120      130      140      150      160      170      180

      220      230      240 X      250      260      270      280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
YCFSVQAVIPSRVTNRKSTDSPVECM
      190      200      X

```

290
NSPL

8. FURN-969863-FIG2.PEP (1-295)
R10065 Newcastle disease virus (NDV) F gene product.

ID R10065 standard; Protein; 553 AA.
AC R10065;
DT 14-MAR-1991 (first entry)
DE Newcastle disease virus (NDV) F gene product.
KW Avipoxvirus; fowlpoxvirus; vaccine.
OS Newcastle disease virus.
PN EP-404576-A.
PD 27-DEC-1990.
PF 21-JUN-1990; 306806.
PR 22-JUN-1989; JP-160157.
PA (JAPG) NIPPON ZEON KK.
PI Yangida N, Saeki S, Okawa S, Knamogawa K, Iritani Y;
PI Sawaguchi K;
DR WPI: 91-001591/01.
DR Q-PSDB; Q10060.
PT Recombinant avipox virus - contg. CDNA coding for Newcastle
PT disease virus in region non-essential for proliferation, used as
PT live vaccine in fowls

CC VII (FVII).
 SQ Sequence 672 BP; 221 A; 137 C; 161 G; 153 T;

Initial Score = 644 Optimized Score = 658 Significance = 35.87
 Residue Identity = 97% Matches = 662 Mismatches = 9
 Gaps = 5 Conservative Substitutions = 0

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150      160      170      180      190      X 200      210
TCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGG
                                |||
                                CCGGGACCACTAATACTGTGG
                                X      10      20

220      230      240      250      260      270      280
CAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCAATC
CAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCAATC
      30      40      50      60      70      80      90

290      300      310      320      330      340      350      360
AAGTCTACTGTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAG
AAGTCTACTGTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAG
      100      110      120      130      140      150      160

370      380      390      400      410      420      430
AGTGTGACCTCACCAGCAGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCGG
AGTGTGACCTCACCAGCAGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCGG
      170      180      190      200      210      220      230

440      450      460      470      480      490      500
CAGGGAATGTGGAGAGCACCAGTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTACC
CAGGGAATGTGGAGAGCACCAGTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTACC
      240      250      260      270      280      290      300      310

510      520      530      540      550      560      570
TGGAGACAAACCTCGGACAGCCAAACATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAG
TGGAGACAAACCTCGGACAGCCAAACATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAG
      320      330      340      350      360      370      380

580      590      600      610      620      630      640
AAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAA
AAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAA
      390      400      410      420      430      440      450

650      660      670      680      690      700      710      720
TTTATACACTTTATTATTGGAATCTTCAAGTTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTT
TTTATACACTTTATTATTGGAATCTTCAAGTTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTT
      460      470      480      490      500      510      520

730      740      750      760      770      780      790
TGATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAACC
TGATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAACC
      530      540      550      560      570      580      590

800      810      820      830      840      850      860
GGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACA-TC
GGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAG-AAATA-ACTGCAGTC
      600      610      620      630      640      650      660

870      880      890      900      910      920
ATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTATCATCCTGGCTATATCTCT
--TAGA
670 X

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7. FURM-969863-FIG2.SEQ (1-987)

043701 Sequence of the human COL1A1 gene extending from i

ID 043701 standard; DNA; 5931 BP.
 AC 043701;
 DT 24-SEP-1993 (first entry)
 DE Sequence of the human COL1A1 gene extending from intron 25 to exon
 DE 52.
 KW Type 1 procollagen; COL1A1; COL2A1; osteoporosis; ss.
 OS Homo sapiens.
 PN W09311149-A.
 PD 10-JUN-1993.
 PF 01-DEC-1992; U10355.
 PR 07-DEC-1991; M8-807428

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170      180      190      200      210      220      230
   310   320   330   340   350   360   370
TCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGACCTCAC
TCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGACCTCAC
240     250     260     270     280     290     300

   380   390   400   410   420   430   440
CGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCCTACCCGGCAGGGAATGTGGA
CGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCCTACCCGGCAGGGAATGTGGA
310     320     330     340     350     360     370     380

   450   460   470   480   490   500   510
GAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCT
GAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCT
390     400     410     420     430     440     450

520     530     540     550     560     570     580     590
CGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGAC
CGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGAC
460     470     480     490     500     510     520

   600   610   620   630   640   650   660
TTTAGTCAGAAGGAACAACACTTTCTTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTA
TTTAGTCAGAAGGAACAACACTTTCTTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTA
530     540     550     560     570     580     590

   670   680   690   700   710   720   730
TTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAACACTAATGAGTTTTTGATTGATGTGGA
TTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAACACTAATGAGTTTTTGATTGATGTGGA
600     610     620     630     640     650     660

   740   750   760   770   780   790   800
TAAAGGAGAAACTACTGTTTCAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGA
TAAAGGAGAAACTACTGTTTCAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGA
670     680     690     700     710     720     730     740

   810   820   830   840   850   860   870
CAGCCCGGTAGAGTGATGAGGCCAGGAGAAAGGGGAATTAGAGAAATATTCTACATCATTGGAGCTGTGGT
CAGCCCGGTAGAGTGATGAGGCCAGGAGAAAGGGGAATTAGAGAAATATTCTACATCATTGGAGCTGTGGT
750     760     770     780     790     X

880     890     900     910
ATTTGTGGTCATCATCCTTGTATCATCCTGGC

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6. FURM-969863-FIG2.SEQ (1-987)
045779 Truncated tissue factor gene.

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ID   Q45779 standard; cDNA; 672 BP.
AC   Q45779;
DT   12-JAN-1994 (first entry)
DE   Truncated tissue factor gene.
KW   Monoclonal antibody; zymogen; rapid; protein isolation; calcium;
KW   presence; fusion protein; affinity chromatography; tTF; ss.
OS   Homo sapiens.
FH   Key                     Location/Qualifiers
FT   CDS                     4..660
FT   /*tag= a
FT   misc_recomb              1..6
FT   /*tag= b
FT   misc_recomb              67..72
FT   /*tag= c
PN   W09313211-A.
PD   08-JUL-1993.
PF   29-DEC-1992; U11270.
PR   03-JAN-1992; US-816679.
PA   (OKLA-) OKLAHOMA MED RES FOUND.
PI   Esmon CT, Morrissey JH, Rezaie A.
DR   WPI; 93-227327/28.
DR   P-PSDB; R39392.
PT   Fusion protein allowing rapid isolation of protein from soln. -
PT   comprises desired protein and epitope recognised by monoclonal
PT   antibody HPC-4
PS   Example 1; Page 24,25; 42pp; English.
CC   The sequence is that encoding truncated tissue factor, the
CC   truncated tissue factor protein lacks the predicted transmembrane
CC   and cytoplasmic domains of tissue factor. The truncated tissue
CC   factor is no longer tethered to the phospholipid membrane surface.
CC   This soluble tissue factor is not a cofactor for precursor factor

```

ACTAATGAGTTTTGATTGATGGATAAAGGAGAAAAGGAGTGTGTTTCAAGCAGTGATTCCTCC
730 740 750 760 770 780 790

790 800 810 820 830 840 850
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
800 810 820 830 840 850 860

860 870 880 890 900 910 920
ATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCTGGCTATATCTCTACAC
ATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCTGGCTATATCTCTACAC
870 880 890 900 910 920 930

930 940 950 960 970 980 X
AAGTGTAGAAAGGAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
AAGTGTAGAAAGGAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCAC
940 950 960 970 980 990 1000

TGTTGGAGCTACTGCAAATGCTATATTGCACTGTGACCGAG
1010 1020 1030 1040

5. FURM-969863-FIG2.SEQ (1-987)
Q29716 Sequence of truncated tissue factor (tTF) cDNA.

ID Q29716 standard; cDNA; 795 BP.
AC Q29716;
DT 02-APR-1993 (first entry)
DE Sequence of truncated tissue factor (tTF) cDNA.
KW Activated factor VII; factor VIIa; truncated tissue factor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1..33
FT /*tag= a
FT CDS 34..130
FT /*tag= b
FT /product= leader peptide
PN WD9218870-A.
PD 29-OCT-1992.
PF 09-APR-1992; U02898.
PR 10-APR-1991; U5-683682.
PA (OKLA-) OKLAHOMA MED RES FOUND.
PI Morrissey JJ;
DR WPI; 92-382277/46.
DR P-PSDB; R28067.
PT Assay for factor VIIa utilising truncated tissue factor - used to
PT monitor factor VIIa therapy in haemophiliac(s), to screen for
PT elevated factor VIIa levels and assess risk of thrombosis
PS Disclosure; Fig 1; 37pp; English.
CC Starting with clone pCTF543 a TF1-219 deletion mutant was
CC constructed that contained the coding sequence for the predicted
CC leader peptide and extracellular domains, but lacked the predicted
CC transmembrane and cytoplasmic domains. This version of the protein
CC retains cofactor activity but fails to support conversion of
CC factor VII to VIIa. The essential difference between truncated
CC tissue factor and wild-type tissue factor is that truncated tissue
CC factor is no longer tethered to the phospholipid membrane surface.
SQ Sequence 795 BP; 234 A; 186 C; 199 G; 176 T;

Initial Score = 781 Optimized Score = 785 Significance = 43.73
Residue Identity = 98% Matches = 786 Mismatches = 9
Gaps = 2 Conservative Substitutions = 0

20 30 40 50 60 X 70 80
GGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCGG
CG--TTCCGCTCGATCTCGCGG
X 10 20

90 100 110 120 130 140 150
CCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCCGTCGCTCGGACGCT
CCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCCGTCGCTCGGACGCT
30 40 50 60 70 80 90

160 170 180 190 200 210 220 230
CCTGCTCGGCTGGGTCTTCGCCCAGGTGGCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTT
CCTGCTCGGCTGGGTCTTCGCCCAGGTGGCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTT
100 110 120 130 140 150 160

240 250 260 270 280 290 300
AACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCAACCCGTCAATCAAGTCTACACTGT
AACTTCAAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCAACCCGTCAATCAAGTCTACACTGT
AACTTCAAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCAACCCGTCAATCAAGTCTACACTGT

FT Sig_peptide 112..207
FT /*tag= a
FT Mat_peptide 208..999
FT /*tag= c
PN EP-347262-A.
PD 20-DEC-1989.
PF 19-JUN-1989; 306176.
PR 17-JUN-1988; US-208895.
PA (UYVA-) Yale Univ, (UYNY-) City Univ New York.
PI Nemerson Y, Konigsberg W;
DR WPI; 89-372479/51.
DR P-PSDB; P93986.
PT Cloning and expression of human tissue factor - for the prodn. of
PT diagnostic reagents, anticoagulant agents and for experimental studies.
PS Disclosure; pp; English.
CC cDNA fragment codes for the entire human tissue factor gene, which may
CC be cloned into plasmid or bacteriophage vectors to produce pure or
CC truncated tissue factor, useful for diagnostic reagents, anticoagulant
CC agents and experimental purposes.
SQ Sequence 2147 BP; 613 A; 455 C; 477 G; 602 T;

Initial Score = 983 Optimized Score = 983 Significance = 55.32
Residue Identity = 99% Matches = 983 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

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      X      10      20      30      40      50      60
      CTGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
CGGGCGAACCCCTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
      10 X      20      30      40      50      60      70
      70      80      90      100     110     120     130
GCCACGGAACCCGCTCGATCTGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
GCCACGGAACCCGCTCGATCTGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
      80      90      100     110     120     130     140
      140     150     160     170     180     190     200
CCCGAGACCGCGCTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
CCCGAGACCGCGCTCGCTCGGAGGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
      150     160     170     180     190     200     210
      210     220     230     240     250     260     270
ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCC
ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCC
      220     230     240     250     260     270     280
      280     290     300     310     320     330     340
AAACCCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAATGCTTTTAC
AAACCCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAATGCTTTTAC
      290     300     310     320     330     340     350     360
      350     360     370     380     390     400     410     420
ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
      370     380     390     400     410     420     430
      430     440     450     460     470     480     490
TTCTCTACCCGGCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAG
TTCTCTACCCGGCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAG
      440     450     460     470     480     490     500
      500     510     520     530     540     550     560
TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTG
TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTG
      510     520     530     540     550     560     570
      570     580     590     600     610     620     630
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
      580     590     600     610     620     630     640
      640     650     660     670     680     690     700
GGCAAGGACTTAATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAAC
GGCAAGGACTTAATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAAC
      650     660     670     680     690     700     710     720
      710     720     730     740     750     760     770     780
ACTAATGAGTTTTTATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGCAGTGATTCCCTCC

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80      90      100     110     120     130     140
150      160      170      180      190      200      210
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
150      160      170      180      190      200      210

220      230      240      250      260      270      280
GCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
GCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
220      230      240      250      260      270      280

290      300      310      320      330      340      350      360
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACA
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACA
290      300      310      320      330      340      350      360

370      380      390      400      410      420      430
GAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCG
GAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCG
370      380      390      400      410      420      430

440      450      460      470      480      490      500
GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTAC
GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTAC
440      450      460      470      480      490      500

510      520      530      540      550      560      570
CTGGAGACAAACCTCGGACAGCCAAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA
CTGGAGACAAACCTCGGACAGCCAAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA
510      520      530      540      550      560      570

580      590      600      610      620      630      640
GAAGATGAACGGACTTTAGTCAGAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA
GAAGATGAACGGACTTTAGTCAGAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA
580      590      600      610      620      630      640

650      660      670      680      690      700      710      720
ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT
ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT
650      660      670      680      690      700      710      720

730      740      750      760      770      780      790
TTGATTGATGTGGATAAAGGAGAAAACACTGTTTCAGTGTTCAAGCAGTGATTCCCTCCCGAACAGTTAAC
TTGATTGATGTGGATAAAGGAGAAAACACTGTTTCAGTGTTCAAGCAGTGATTCCCTCCCGAACAGTTAAC
730      740      750      760      770      780      790

800      810      820      830      840      850      860
CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC
CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC
800      810      820      830      840      850      860

870      880      890      900      910      920      930
ATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATCTTACACAAGTGTAGAAAG
ATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATCTTACACAAGTGTAGAAAG
870      880      890      900      910      920      930

940      950      960      970      980      X
GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCACTGTTGGAGCTAC
940      950      960      970      980      990      1000

TGCAATGCTATATTGCACTGTGACCGAG
1010      1020      1030

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4. FURM-969863-FIG2.SEQ (1-987)
N92782 cDNA of entire human tissue factor apoprotein.

ID N92782 standard; cDNA; 2147 BP.
AC N92782;
DT 22-MAY-1990 (first entry)
DE cDNA of entire human tissue factor apoprotein.
KW Human tissue factor; coagulation system; anticoagulant; ds.
OS Homo sapiens.
EU

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GGCAAGGACTTAATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAAC
650      660      670      680      690      700      710      720
710      720      730      740      750      760      770      780
ACTAATGAGTTTTTGTGATTGATGTGGATAAAGGAGAAAAGTACTGTTTCAGTGTTCAGCAGTGATTCCCTCC
ACTAATGAGTTTTTGTGATTGATGTGGATAAAGGAGAAAAGTACTGTTTCAGTGTTCAGCAGTGATTCCCTCC
730      740      750      760      770      780      790
790      800      810      820      830      840      850
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
800      810      820      830      840      850      860
860      870      880      890      900      910      920
ATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTCTATCTCTACAC
ATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTCTATCTCTACAC
870      880      890      900      910      920      930
930      940      950      960      970      980      X
AAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
AAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCAC
940      950      960      970      980      990      1000
TGTGGAGCTACTGCAATGCTATATTGCACTGTGACCGAG
1010      1020      1030      1040

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3. FURM-969863-FIG2.SEQ (1-987)
N81104 Sequence of human tissue factor protein (TFP) clone

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ID   N81104 standard; DNA; 2127 BP.
AC   N81104;
DT   19-NOV-1990 (first entry)
DE   Sequence of human tissue factor protein (TFP) clone derived from
DE   adipose cDNA library
KW   Hybridisation; coagulation; blood clotting; therapy; ds.
OS   Homo sapiens.
FH   Key          Location/Qualifiers
FT   sig_peptide  100..195
FT   /*tag= a
FT   mat_peptide  196..987
FT   /*tag= b
PN   EP-278776-A.
PD   17-AUG-1988.
PF   12-FEB-1988; 301190.
PR   7-APR-1987; US-035409..
PR   05-FEB-1988; US-152698.
PA   (GETH) Genentech Inc.
PI   Lawn RM, Wion KL, Vehar GA;
DR   WPI; 88-229602/33.
DR   P-PSDB; P80504.
PT   Tissue factor protein and derivs. -
PT   obtd. by recombinant deoxyribonucleic acid techniques, used to
PT   treat chronic bleeding and coagulation-disorders
PS   Claim 4; Fig 2a-2b; 39pp; English.
CC   Tissue factor protein (TFP) free of substances from its natural source is
CC   claimed. TFP administered to provide a coagulation inducing therapeutic
CC   compsn. for various chronic bleeding disorders. Two oligo probes
CC   representing one possible codon choice for each AA of the N-terminal AA
CC   sequence (60 nucleotides) and internal AA sequence near the C-terminal
CC   (81 nucleotides) were designed and synthesised. cDNA clones of human TFP
CC   were obtd. using the DNA probes first to screen a human placental cDNA
CC   library. 1400 BP EcoRI fragment from a placental clone was used to screen
CC   a human adipose cDNA library. The full length human TFP cDNA was contd.
CC   within the cDNA clone lambda TF14. The full length cDNA was inserted into
CC   an expression plasmid and TFP was expressed using mammalian cells (COS)
CC   cells and E.coli.
SQ   Sequence 2127 BP; 606 A; 450 C; 472 G; 599 T;

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Initial Score = 987 Optimized Score = 987 Significance = 55.55
Residue Identity = 100% Matches = 987 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

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X      10      20      30      40      50      60      70
CTCGCACTCCCTCTGGCCGCGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
|||||
CTCGCACTCCCTCTGGCCGCGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
X      10      20      30      40      50      60      70

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```

80      90      100      110      120      130      140
GCTCGATCTCGCCGCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC
GCTCGATCTCGCCGCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC

```

FT /*tag= a
FT /product=human tissue factor
FT sig_peptide 112..207
FT /*tag= b
FT mat_peptide 208..996
FT /*tag= c
FT /product=apoprotein
PN W08809817-A.
PD 15-DEC-1988.
PF 08-JUN-1988; U01915.
PR 2-JUN-1986; US-062166.
PR 14-MAR-1988; US-167870.
PA (MOUN-) Mount Sinai Sch Med, (UYVA-) Yale University,
PA (UYNY-) City Univ New York, (MOUN) Mount Sinai Hosp Res Fdn.
PI Menerson Y, Konigsberg W;
DR WPI; 88-368631/51.
PT New recombinant cloning vehicle expressing human tissue factor -
PT encoding DNA sequences, transformed cells and pure apoprotein
PT prods
PS Disclosure; pp; English.
CC The fragment encodes a single chain polypeptide preprotein 295
CC long. The signal sequence is post translationally cleaved to give
CC a mature protein of 263 amino acids.
CC HTF can be used for inhibiting binding of factor VIII to tissue
CC factor.
CC See also N81950-2.
SQ Sequence 2147 BP; 613 A; 454 C; 477 G; 603 T;

Initial Score = 987 Optimized Score = 987 Significance = 55.55
Residue Identity = 100% Matches = 987 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      CTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
CGGGCGAACCCCTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
10  X      20      30      40      50      60      70
      70      80      90      100     110     120     130
      GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
      GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
      80      90      100     110     120     130     140
      140     150     160     170     180     190     200
      CCGGACACCGCGTGCCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
      CCGGACACCGCGTGCCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
      150     160     170     180     190     200     210
      210     220     230     240     250     260     270
      ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCC
      ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCC
      220     230     240     250     260     270     280
      280     290     300     310     320     330     340
      AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC
      AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC
      290     300     310     320     330     340     350     360
      350     360     370     380     390     400     410     420
      ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
      ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
      370     380     390     400     410     420     430
      430     440     450     460     470     480     490
      TTCTCTACCCGGCAGGGAATGTGGAGAGACCCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAG
      TTCTCTACCCGGCAGGGAATGTGGAGAGACCCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAG
      440     450     460     470     480     490     500
      500     510     520     530     540     550     560
      TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTGAACAGGTGGGAACAAAAGTG
      TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTGAACAGGTGGGAACAAAAGTG
      510     520     530     540     550     560     570
      570     580     590     600     610     620     630
      AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
      AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
      580     590     600     610     620     630     640
      640     650     660     670     680     690     700
      GCGAAGCACTTAATTTATACACTTTATTATTGAAATCTTCAAGTTCAGGAAAGCAAAACACCAAAACAAAC
```

```

170      180      190      200      210      220      230
GCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACTTGA
|||
GCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACTTGA
230      240      250      260      270      280      290

240      250      260      270      280      290      300      310
AATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTAATCAAGTCTACACTGTTCAAATAA
|||
AATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTAATCAAGTCTACACTGTTCAAATAA
300      310      320      330      340      350      360      370

320      330      340      350      360      370      380
GCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAGAGTGTGACCTCACCAGCAGAGA
|||
GCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAGAGTGTGACCTCACCAGCAGAGA
380      390      400      410      420      430      440

390      400      410      420      430      440      450
TTGTGAAGGATGTGAAGCAGACGTAAGTGGCACGGGCTTCTCTCTACCCGGCAGGGAATGTGGAGAGCACCG
|||
TTGTGAAGGATGTGAAGCAGACGTAAGTGGCACGGGCTTCTCTCTACCCGGCAGGGAATGTGGAGAGCACCG
450      460      470      480      490      500      510

460      470      480      490      500      510      520
GTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCTCGGACAGC
|||
GTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCTCGGACAGC
520      530      540      550      560      570      580

530      540      550      560      570      580      590
CAACAATTCAGAGTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCA
|||
CAACAATTCAGAGTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCA
590      600      610      620      630      640      650

600      610      620      630      640      650      660      670
GAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGA
|||
GAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGA
660      670      680      690      700      710      720      730

680      690      700      710      720      730      740
AATCTTCAAGTTTCAAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTTGATTGATGTGGATAAAGGAG
|||
AATCTTCAAGTTTCAAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTTGATTGATGTGGATAAAGGAG
740      750      760      770      780      790      800

750      760      770      780      790      800      810
AAACTACTGTTTCAAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGG
|||
AAACTACTGTTTCAAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGG
810      820      830      840      850      860      870

820      830      840      850      860      870      880
TAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGG
|||
TAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGG
880      890      900      910      920      930      940

890      900      910      920      930      940      950
TCATCATCCTTGTATCATCCTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGA
|||
TCATCATCCTTGTATCATCCTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGA
950      960      970      980      990      1000      1010

960      970      980      X
AGGAGAACTCCCCACTGAATGTTTCATAA
|||
AGGAGAACTCCCCACTGAATGTTTCATAAAGGAAGCACTGTTGAGCTACTGCAAATGCTATATTGCACTGT
1020      1030      1040      1050      1060      1070      1080      1090
GACCGAG

```

2. FURM-969863-FIG2.SEQ (1-987)

N81953 Encodes human tissue factor

ID N81953 standard; cDNA; 2147 BP.
AC N81953;
DT 22-OCT-1990 (first entry)
DE Encodes human tissue factor
KW human tissue factor (HTF) apoprotein; procoagulant;
KW Factor VIII; ss.
OS synthetic.
FH Key Location/Qualifiers
ET cns 112..999

11.	Q20269	Gene encoding AE-III (peptidyl	3383	114	427	5.45	0
12.	Q25107	DHFR-APP fusion protein (pBBK	4670	112	416	5.34	0
13.	Q22995	Sequence encoding 53 kD cellu	1182	110	420	5.22	0
14.	Q11563	Encodes E-cadherin from dog k	4333	110	432	5.22	0
15.	Q39967	PKC-alpha cDNA.	3305	107	432	5.05	0
16.	N40141	Sequence of human factor IX g	11866	107	402	5.05	0
17.	N40176	Sequence of human factor IX g	11873	107	401	5.05	0
*** 4 standard deviations above mean ***							
18.	N60202	Interferon-pseudo-oncogene-2.	2132	105	420	4.94	0
19.	Q13802	Non-receptor linked protein t	2287	105	385	4.94	0
20.	Q03661	Maize C3 sequence encoding ac	2546	105	421	4.94	0
21.	Q10543	BamHI J-I fragment carrying s	2721	104	395	4.88	0
22.	Q10212	BamHI J-I fragment carrying s	2721	104	395	4.88	0
23.	N50525	Bacillus thuringiensis var. i	3756	104	422	4.88	0
24.	Q32366	MAGE-10 genomic DNA.	920	102	259	4.76	0
25.	N81341	Recombinant plasmid pMP1 cont	4133	102	409	4.76	0
26.	N71017	Sequence of LAV/HTLV III gag	5340	102	431	4.76	0
27.	N60142	Sequence of ARV-2 cloned in p	2467	101	324	4.71	0
28.	Q31938	p41 gag gene (fusion of p25 g	2467	100	323	4.65	0
29.	Q13673	SUP-B27 t(1;19) translocation	2837	99	422	4.59	0
30.	Q13675	E2A/pr1 fusion transcript fro	2922	99	421	4.59	0
31.	Q49757	pTK gene HpTK5.	3969	99	409	4.59	0
32.	Q45503	Sequence encoding an antibody	1657	98	356	4.53	0
33.	Q24174	M13IX421.	7294	98	415	4.53	0
34.	Q24172	M13IX30.	7445	98	414	4.53	0
35.	Q14752	HIV-1(MN-ST1) env protein-enc	9746	98	428	4.53	0
36.	Q12528	Thymidylate phosphohydrolase.	1611	97	354	4.48	0
37.	Q27487	PT42 promoter and 5' gene por	2370	97	382	4.48	0
38.	Q24171	M13IX22.	7320	97	411	4.48	0
39.	Q33150	CAT-LacZ alpha-peptide trans-	623	96	243	4.42	0
40.	Q27243	CAT-LacZ alpha-peptide trans-	623	96	243	4.42	0

1. FURM-969863-FIG2.SEQ (1-987)
Q20349 Thromboplastin clone 2b-Apr5.

ID Q20349 standard; cDNA; 2189 BP.
AC Q20349;
DT 09-APR-1992 (first entry)
DE Thromboplastin clone 2b-Apr5.
KW Thromboplastin; Ig; fusion protein; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 160..1044
FT /*tag= a
FT /label= thromboplastin
PN EP-464533-A.
PD 08-JAN-1992.
PF 24-JUN-1991; 110368.
PR 28-JUN-1990; DE-020607.
PA (BEHW) BEHRINGWERKE AG.
PA (GEHO-) GENERAL HOSPITAL CORP.
PI Laufer L, Oquendo P, Zettlmeiss G, Seed B;
DR WPI; 92-009794/02.
PT Soluble fusion protein useful in treatment or diagnosis - contg.
PT immunoglobulin constant region and e.g. thromboplastin, cytokine
PT or receptor, expressed in mammalian cells
PS Disclosure; Fig 2; 21pp; German.
CC Based on the thromboplastin DNA sequence published by Scarpati et al.,
CC Biochemistry, Bd. 26 (1987), 5234-5238, two oligonucleotide probes
CC are derived (Q20350-51). A human placenta cDNA bank is screened.
CC Several clones are obtained and clone 2b-Apr5 is isolated. The derived
CC amino acid sequence is as described by Scarpati et al.
CC See also Q20349-57.
SQ Sequence 2189 BP; 617 A; 470 C; 487 G; 615 T;

Initial Score = 987 Optimized Score = 987 Significance = 55.55
Residue Identity = 100% Matches = 987 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

                                X      10      20
                                CTGCACTCCCTCTGGCCGGCC
GAGGTCGACGGTATCGATAAGCTTGATATCGAATTCTCTCGGCGAACCCCTCGCACTCCCTCTGGCCGGCC
      20      30      40      50      60      70      80

      30      40      50      60      70      80      90
CAGGGGCGCCTTCAGCCCAACCTCCCGAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGG
CAGGGGCGCCTTCAGCCCAACCTCCCGAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGG
      90     100     110     120     130     140     150

     100     110     120     130     140     150     160
TAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGTCTGCTCGGACGCTCCTGCTCG
TAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGTCTGCTCGGACGCTCCTGCTCG
     160     170     180     190     200     210     220

```

#authors Hartzels, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
 #journal Mol. Cell. Biol. (1989) 9:2567-2573
 #title A growth factor-responsive gene of murine BALB/c 3T3 cells
 encodes a protein homologous to human tissue factor.
 #cross-references MUID:89343974
 #accession A32318
 ##molecule_type mRNA
 ##residues 1-294 ##label HAR
 ##cross-references GB:M26071
 REFERENCE A39046
 #authors Ranganathan, G.; Blatti, S.P.; Subramanian, M.; Fass, D.N.;
 Maihle, N.J.; Getz, M.J.
 #journal J. Biol. Chem. (1991) 266:496-501
 #title Cloning of murine tissue factor and regulation of gene
 expression by transforming growth factor type beta1.
 #cross-references MUID:91093171
 #accession A39046
 ##molecule_type mRNA
 ##residues 1-25, 'I', 27-294 ##label RAN
 ##cross-references GB:J05713
 ##note 26-Thr was also found
 COMMENT Tissue factor is an integral membrane glycoprotein that serves as a
 receptor for plasma coagulation factor VIIa. The complex
 initiates the extrinsic coagulation pathway.
 COMMENT Expression of tissue factor can be induced in a variety of tissues
 by certain growth factors and inflammatory stimuli.
 CLASSIFICATION #superfamily tissue factor
 KEYWORDS blood coagulation; glycoprotein; membrane protein
 FEATURE
 1-29 #domain signal sequence #status predicted #label SIG
 30-294 #protein tissue factor #status predicted #label MAT
 30-251 #domain extracellular #status predicted #label EXT
 252-274 #domain transmembrane #status predicted #label TM
 75-83,218-241 #disulfide_bonds #status predicted
 37,57,169,200 #binding_site carbohydrate (Asn) (covalent) #status
 predicted
 275 #binding_site fatty acid (Cys) (covalent) #status
 experimental
 SUMMARY #length 294 #molecular-weight 32923 #checksum 9197
 SEQUENCE

Initial Score = 87 Optimized Score = 219 Significance = 5.50
 Residue Identity = 52% Matches = 158 Mismatches = 114
 Gaps = 13 Conservative Substitutions = 16

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKVSTNFKTIIEWEPKPVNQVYTVQIST
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
MAILVRPRL---AALAPT-FLGCLLLQVTAGAGIPEK--AFNLTWISTDFKTIIEWQPKPTNYTYTVQISD
X      10      20      30      40      50      60

      80      90     100     110     120     130
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYP-AGNVESTGS-----AGEPLYENSPEFTPYLET
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RSRNWKNKCFSTTDTTECDLTDEIVKDVWYAEAKVLSVPRNSVHGDGDQLVIHGEEPPFTNAPKFLPYRDT
70      80      90     100     110     120     130

140     150     160     170     180     190     200     210
NLGQPTIQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYLYWKSSSSGKKTAKTNTNEFLID
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
NLGQPVIIQFEQDGRKLNVVVKDSLTLVRKNGFTLRLQVFGKDLGYIITYRKGSSTGKKTNTITNEFSID
140     150     160     170     180     190     200     210

220     230     240     250     260     270     280
VDKGENYCFVSQAVIPSRVTNRKSTDSPVECMGQEGEFREIFYIIGAVVFVVIILVILAIHLKCRKAGV
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
VEEGVSYCFVQAMIFSRKTQNSPGSSTVCTEQWKSFLGETLIIVGAVVLLATIFIILLSISLCKRRKNRA
220     230     240     250     260     270     280

290 X
GQSMKENSPLNVS
| | | | |
GQKGG-NTPSRLA
290 X
  
```

8. FURM-969863-FIG2.PEP (1-295)
 VGNZU1 fusion glycoprotein - Newcastle disease virus (str

ENTRY VGNZU1 #type complete
 TITLE fusion glycoprotein - Newcastle disease virus (strain Ulster)
 ORGANISM #formal name Newcastle disease virus
 DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
 30-Jun-1993
 ACCESSIONS A29823
 REFERENCE A92799
 #authors Millar, N.S.; Chambers, P.; Emerson, P.T.
 #journal J. Gen. Virol. (1989) 70:117-120

```

IQSFEQVGTKLVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
150      160      170      180      190      200      210
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
220      230      240      250      260      270      280
YCFSVQAVIPSRKRKRQSPESLTCTSRQGRAREMFFIIGAVV-VVALLIIVLSVTVYKCRKARACPSGKE
220      230      240      250      260      270      280
290      X
NSPLNVS
||||::
SSPLNIA
290      X

```

6. FURM-969863-FIG2.PEP (1-295)

S23681 tissue factor - rabbit

```

ENTRY      S23681      #type complete
TITLE      tissue factor - rabbit
ORGANISM    #formal name Oryctolagus cuniculus #common_name domestic
              rabbit
DATE        22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
              22-Nov-1993
ACCESSIONS  S23681
REFERENCE   S23681
#authors    Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.;
              Konigsberg, W.
#journal     Thromb. Haemost. (1991) 66:315-320
#title       Molecular cloning, characterization and expression of cDNA
              for rabbit brain tissue factor.
#cross-references MUID:92081032
#accession    S23681
##status      preliminary
##residues     1-260 ##label PAW
##cross-references EMBL:X53521
SUMMARY      #length 260 #molecular-weight 29312 #checksum 2601
SEQUENCE

```

Initial Score = 209 Optimized Score = 229 Significance = 5.88
 Residue Identity = 71% Matches = 186 Mismatches = 56
 Gaps = 1 Conservative Substitutions = 18

```

10      20      30      X      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEKPVNQVYTVQIST
ADTTGRAYNLTKWSTNFKTILEWEKPSIDHVVYTVQIST
X      10      20      30
80      90      100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
RLENWKKSCFLTAETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPT
40      50      60      70      80      90      100     110
150     160     170     180     190     200     210
IQSFEQVGTKLVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
120     130     140     150     160     170     180
IQSFEQVGTKLVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
190     200     210     220     230     240     250
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
YCFSVQAVIPSRKRKRQSPESLTCTSRQGRAREMFFIIGAVV-VVALLIIVLSVTVYKCRKARACPSGKE
190     200     210     220     230     240     250

```

```

290      X
NSPLNVS
||||::
SSPLNIA
260

```

7. FURM-969863-FIG2.PEP (1-295)

KFMS3 tissue factor precursor - mouse

```

ENTRY      KFMS3      #type complete
TITLE      tissue factor precursor - mouse
ALTERNATE_NAMES coagulation factor III
ORGANISM    #formal name Mus musculus #common_name house mouse
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
              30-Sep-1993
ACCESSIONS  A32318; A39046
REFERENCE   A32318

```

```

      80          90          100         110         120         130         140
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RLGNHKNKCFYTTNTECDVTDIVKNVRETYLARVLSYPA---DTSSSTVEPPFTNSPEFTPYLETNLGQPT
      80          90          100         110         120         130         140

      150         160         170         180         190         200         210
IQSFGEVGTKNVNTVEDERTLVRNRNNTFLSLRDVFGKDLIYTLVYWKSSSSGKKTAKTNTNEFLIDVDKGEN
:|||||:|||||:|||||:|||||:|||||:|||||:|||||
IQSFGEVGTKNLNTVQDARTLVRANS AFLSLRDVFGKDLNNTLVYWKASSTGKKKATTNTNGFLIDVDKGEN
      150         160         170         180         190         200         210

      220         230         240         250         260         270         280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
:|||||:|||||:|||||:|||||:|||||:|||||:|||||
YCFHVGAVILSRRVNGKSPESPIKTSHERVLSTELFFIIGTVMVLVIIIFIVVLSVSLHKCRKVRAERSGKE
      220         230         240         250         260         270         280

290 X
NSPLNVS
:|||||:
NTPLNAA
290 X

```

5. FURM-969863-F1G2.PEP (1-295)

KFRB3 tissue factor precursor - rabbit

```

ENTRY          KFRB3          #type complete
TITLE          tissue factor precursor - rabbit
ALTERNATE_NAMES coagulation factor III
ORGANISM       #formal name Oryctolagus cuniculus #common_name domestic
               rabbit
DATE          30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
               30-Sep-1993
ACCESSIONS     JU0441
REFERENCE      JU0441
#authors       Andrews, B.S.; Rehentulla, A.; Fowler, B.J.; Edgington, T.S.;
               Mackman, N.
#journal       Gene (1991) 98:265-269
#title         Conservation of tissue factor primary sequence among three
               mammalian species.
#cross-references NUID:91200676
#contents      brain
#accession     JU0441
##molecule_type mRNA
##residues     1-292 ##label AND
##cross-references GB:M55390
COMMENT        Tissue factor is an integral membrane glycoprotein that serves as a
               receptor for plasma coagulation factor VIIa. The complex
               initiates the extrinsic coagulation pathway.
COMMENT        Expression of tissue factor can be induced in a variety of tissues
               by certain growth factors and inflammatory stimuli.
CLASSIFICATION #superfamily tissue factor
KEYWORDS       blood coagulation; glycoprotein; membrane protein
FEATURE
1-32           #domain signal sequence #label SIG
33-292         #protein tissue factor #label MAT
33-249         #domain extracellular #status predicted #label EXT
250-271        #domain transmembrane #status predicted #label TMM
272-292        #domain intracellular #status predicted #label INT
79-87,216-239  #disulfide_bonds #status predicted
41,114,154,167,
182            #binding_site carbohydrate (Asn) (covalent) #status
               predicted
274            #binding_site fatty acid (Cys) (covalent) #status
               experimental
SUMMARY        #length 292 #molecular-weight 32738 #checksum 1871
SEQUENCE

```

```
Initial Score      = 209  Optimized Score = 254  Significance = 6.80
Residue Identity  = 69%  Matches       = 206  Mismatches  = 67
Gaps              = 3    Conservative Substitutions = 19
```

X
METPAWPRVPRPETAVARTLLLGWVFAQVAGASCTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
MAPPTRLQVPRPGTAVPYTVLLGWLLAGVARAADTTGR--AYNLTKWSTNFKTILEWEPKSIDHVYTVQIST
X
10 20 30 40 50 60 70
10 20 30 40 50 60 70

80 90 100 110 120 130 140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
:
RLENWKSCKFLTAETECDLTDEVVKDVGGTYMARVLSYPARNNGNTTFPEEPPFRNSPEFTPYLDTNLGQPT
80 90 100 110 120 130 140

Residue Identity = 100% Matches = 295 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X
```

4. FURM-969863-FIG2.PEP (1-295)

KFB03 tissue factor precursor - bovine

```
ENTRY      KFB03      #type complete
TITLE      tissue factor precursor - bovine
ALTERNATE_NAMES coagulation factor III
ORGANISM    #formal_name Bos primigenius taurus #common_name cattle
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
            30-Sep-1993
ACCESSIONS  J01319
REFERENCE   J01319
#authors    Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
#journal     Biochem. Biophys. Res. Commun. (1991) 181:1145-1150
#title       cDNA and amino acid sequences of bovine tissue factor.
#cross-references MUID:92109720
#contents    Adrenal gland
#accession   J01319
##molecule_type mRNA
##residues   1-292 ##label TAK
##cross-references GB:S74147
##note       part of this sequence, including the amino end of the
              mature protein, was confirmed by protein sequencing
COMMENT     Tissue factor is an integral membrane glycoprotein that serves as a
              receptor for plasma coagulation factor VIIa. The complex
              initiates the extrinsic coagulation pathway.
COMMENT     Expression of tissue factor can be induced in a variety of tissues
              by certain growth factors and inflammatory stimuli.
CLASSIFICATION #superfamily tissue factor
KEYWORDS      blood coagulation; glycoprotein; membrane protein
FEATURE
1-35          #domain signal sequence #label SIG
36-292        #protein tissue factor #status experimental #label MAT
36-248        #domain extracellular #status predicted #label EXT
249-271       #domain transmembrane #status predicted #label TMM
272-292       #domain intracellular #status predicted #label INT
81-89,215-238 #disulfide bonds #status predicted
43,153,181    #binding_site carbohydrate (Asn) (covalent) #status
              predicted
118,124       #binding_site carbohydrate (Thr) (covalent) #status
              predicted
274          #binding_site fatty acid (Cys) (covalent) #status
              experimental
SUMMARY      #length 292 #molecular-weight 32475 #checksum 1836
SEQUENCE
```

Initial Score = 148 Optimized Score = 257 Significance = 6.92
Residue Identity = 69% Matches = 204 Mismatches = 71
Gaps = 3 Conservative Substitutions = 17

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X
```

290 X
 NSPLNVS
 |||||
 NSPLNVS
 290 X

3. FURM-969863-FIG2.PEP (1-295)

KFHU3 tissue factor precursor - human

ENTRY KFHU3 #type complete
 TITLE tissue factor precursor - human
 ALTERNATE_NAMES coagulation factor III
 ORGANISM #formal name Homo sapiens #common name man
 DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
 03-Feb-1994
 ACCESSIONS A28320; A29062; A29672; A29008
 REFERENCE A74171
 #authors Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams,
 K.R.; Guha, A.; Kraus, J.; Lin, T.C.; Nemerson, Y.;
 Konigsberg, W.H.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:5148-5152
 #title Isolation of cDNA clones coding for human tissue factor:
 primary structure of the protein and cDNA.
 #cross-references MUID:87260946
 #accession A28320
 ##molecule_type mRNA
 ##residues 1-295 ##label SPI
 ##cross-references GB:J02931
 REFERENCE A29062
 #authors Morrissey, J.H.; Fakhrai, H.; Edgington, T.S.
 #journal Cell (1987) 50:129-135
 #title Molecular cloning of the cDNA for tissue factor, the cellular
 receptor for the initiation of the coagulation protease
 cascade.
 #cross-references MUID:87244317
 #accession A29062
 ##molecule_type mRNA
 ##residues 1-295 ##label MOR
 ##cross-references GB:J02931
 #note part of this sequence, including the amino end of the
 mature protein, was confirmed by protein sequencing
 REFERENCE A29672
 #authors Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.;
 Flandermeyer, R.R.; Siegel, N.R.; Sadler, J.E.
 #journal Biochemistry (1987) 26:5234-5238
 #title Human tissue factor: cDNA sequence and chromosome
 localization of the gene.
 #cross-references MUID:88050796
 #accession A29672
 ##molecule_type mRNA
 ##residues 1-259, 'A', 261-295 ##label SCA
 ##cross-references GB:M16553
 REFERENCE A37422
 #authors Bach, R.; Konigsberg, W.H.; Nemerson, Y.
 #journal Biochemistry (1988) 27:4227-4231
 #title Human tissue factor contains thioester-linked palmitate and
 stearate on the cytoplasmic half-cystine.
 #contents annotation; disulfide bonds and fatty acid binding site
 COMMENT Tissue factor is an integral membrane glycoprotein that serves as a
 receptor for plasma coagulation factor VIIa. The complex
 initiates the extrinsic coagulation pathway.
 COMMENT Expression of tissue factor can be induced in a variety of tissues
 by certain growth factors and inflammatory stimuli.
 GENETICS
 #gene GDB:F3
 #map position 1p22-p21
 CLASSIFICATION #superfamily tissue factor
 KEYWORDS blood coagulation; glycoprotein; lipoprotein; membrane
 protein
 FEATURE
 1-32 #domain signal sequence #status experimental #label SIG
 33-295 #protein tissue factor #status experimental #label MAT
 33-251 #domain extracellular #status predicted #label EXT
 252-274 #domain transmembrane #status predicted #label TMM
 275-295 #domain intracellular #status predicted #label INT
 81-89,218-241 #disulfide bonds #status experimental
 43 #binding_site carbohydrate (Asn) (covalent) #status
 experimental
 156,169 #binding_site carbohydrate (Asn) (covalent) #status
 predicted
 277 #binding_site fatty acid (Cys) (covalent) #status
 experimental
 SUMMARY #length 295 #molecular-weight 33067 #checksum 4014
 SEQUENCE

Initial Score = 295 Ontiaized Score = 295 Significance = 8.33

SUMMARY #length 295 #molecular-weight 33067 #checksum 4014
SEQUENCE

Initial Score = 295 Optimized Score = 295 Significance = 8.33
Residue Identity = 100% Matches = 295 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X
```

2. FURM-969863-FIG2.PEP (1-295)

A43645 tissue factor - human

ENTRY A43645 #type complete
TITLE tissue factor - human
ORGANISM #formal name Homo sapiens #common name man
DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
ACCESSIONS A43645
REFERENCE A43645
#authors Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
#journal Biochemistry (1989) 28:1755-1762
#title Complete sequence of the human tissue factor gene, a highly regulated cellular receptor that initiates the coagulation protease cascade.
#accession A43645
##status preliminary
##molecule_type DNA
##residues 1-295 ##label MAC
##cross-references GB:J02844; GB:J02846
SUMMARY #length 295 #molecular-weight 33067 #checksum 4014
SEQUENCE

Initial Score = 295 Optimized Score = 295 Significance = 8.33
Residue Identity = 100% Matches = 295 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280
```

```
ENTRY          A47574          #type complete
TITLE          tissue factor precursor - human
ORGANISM       #formal name Homo sapiens #common name man
DATE           31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                31-Dec-1993
ACCESSIONS     A47574
REFERENCE      A47574
               #authors       Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn,
               R.M.
               #journal       Thromb. Res. (1987) 48:89-99
               #title         Cloning and expression of human tissue factor cDNA.
               #accession     A47574
               ##status       preliminary
               ##molecule_type mRNA
               ##residues      1-295 ##label FIS
               ##cross-references CR:M27474
```

Times: CPU Total Elapsed
00:01:33.96 00:03:13.00

Number of residues: 1520603
Number of sequences optimized: 3760

The scores below are sorted by optimized score.
Significance is calculated based on optimized score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. TF_HUMAN	TISSUE FACTOR PRECURSOR (TF)	295	295	295	61.80	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
2. TF_BOVIN	**** 46 standard deviations above mean **** TISSUE FACTOR PRECURSOR (TF)	292	148	257	46.15	0
3. TF_RABIT	**** 44 standard deviations above mean **** TISSUE FACTOR PRECURSOR (TF)	292	209	254	44.91	0
4. TF_MOUSE	**** 30 standard deviations above mean **** TISSUE FACTOR PRECURSOR (TF)	294	87	219	30.49	0
5. VGLF_NDV0	**** 4 standard deviations above mean **** FUSION GLYCOPROTEIN PRECURSOR	553	7	157	4.94	0
6. VGLF_NDVU	FUSION GLYCOPROTEIN PRECURSOR	553	7	157	4.94	0
7. BRAZ_PSEAE	BRANCHED CHAIN AMINO ACID TRA	437	6	156	4.53	0
8. VGLF_NDVH4	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
9. VGLF_NDVA	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
10. VGLF_NDVT	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
11. VGLF_NDVH3	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
12. VGLX_HSVEB	GLYCOPROTEIN X PRECURSOR.	797	8	156	4.53	0
13. ADP1_MYCGE	140 KD ADHESIN PRECURSOR (ATT	1444	7	155	4.12	0
14. OCT1_HUMAN	OCTAMER-BINDING TRANSCRIPTION	743	7	155	4.12	0
15. VGLF_NDVB	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
16. VGLF_NDVTG	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
17. VGLF_NDVM	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
18. VGLF_NDVL	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
19. VGLF_NDVI	**** 3 standard deviations above mean **** FUSION GLYCOPROTEIN PRECURSOR	553	7	154	3.71	0
20. CYAA_BORPE	CALMODULIN-SENSITIVE ADENYLAT	1706	7	154	3.71	0
21. ASG2_ECOLI	L-ASPARAGINASE II PRECURSOR (348	6	154	3.71	0
22. I230_MOUSE	INDOLEAMINE 2,3-DIOXYGENASE (407	6	153	3.30	0
23. P60_HUMAN	MITOCHONDRIAL MATRIX PROTEIN	573	8	153	3.30	0
24. P60_RAT	MITOCHONDRIAL MATRIX PROTEIN	573	9	153	3.30	0
25. P60_CRIGR	MITOCHONDRIAL MATRIX PROTEIN	573	9	153	3.30	0
26. A4_DROME	BETA-AMYLOID-LIKE PROTEIN PRE	886	7	153	3.30	0
27. P60_MOUSE	MITOCHONDRIAL MATRIX PROTEIN	573	9	153	3.30	0
28. INV4_VERPS	INVASIN.	985	7	153	3.30	0
29. ATC1_YEAST	**** 2 standard deviations above mean **** CALCIUM-TRANSPORTING ATPASE 1	950	7	152	2.88	0
30. FTSZ_BACSU	CELL DIVISION FTSZ PROTEIN.	382	7	152	2.88	0
31. SYFB_BACSU	PHENYLALANYL-TRNA SYNTHETASE	804	7	152	2.88	0
32. MAPB_MOUSE	MICROTUBULE-ASSOCIATED PROTEI	2464	7	152	2.88	0
33. PEC1_HUMAN	PLATELET ENDOTHELIAL CELL ADH	738	7	152	2.88	0
34. AROA_KLEPN	3-PHOSPHOSHIKIMATE 1-CARBOXYV	427	6	152	2.88	0
35. VS14_TRYBB	VARIANT SURFACE GLYCOPROTEIN	514	8	152	2.88	0
36. CH60_BACSU	60 KD CHAPERONIN (PROTEIN CPN	544	7	151	2.47	0
37. CH60_THEP3	60 KD CHAPERONIN (HEAT SHOCK	538	7	151	2.47	0
38. MOT1_YEAST	PROBABLE HELICASE MOT1.	1867	8	151	2.47	0
39. FLIF_BACSU	FLAGELLAR M-RING PROTEIN (FLA	536	7	151	2.47	0
40. ICEN_PSESY	ICE NUCLEATION PROTEIN.	1200	8	151	2.47	0

1. FURM-969863-FIG2.PEP (1-295)
TF_HUMAN TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF HUMAN STANDARD; PRT; 295 AA.
AC P13726;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
GN F3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RM 89247359
RA MACKMAN N. MORRISSEY J. H. FOWLER B. EDINGTON T. S.:

RL BIOCHEMISTRY 28:1755-1762(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RM 87260946
 RA SPICER E.K., HORTON R., BLOEM L., BACH R., WILLIAMS K.R., GUHA A.,
 RA KRAUS J., LIN T.C., NEMERSON Y., KONIGSBERG W.H.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:5148-5152(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RM 87244317
 RA MORRISSEY J.H., FAKHRAI H., EDGINGTON T.S.;
 RL CELL 50:129-135(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RM 88050796
 RA SCARPATI E.M., WEN D., BROZE G.J. JR., MILETICH J.P.,
 RA FLANDERMEYER R.R., SIEGEL N.R., SADLER J.E.;
 RL BIOCHEMISTRY 26:5234-5238(1987).
 RN [5]
 RP DISULFIDE BONDS, AND PALMITOYLATION.
 RM 89000604
 RA BACH R., KONIGSBERG W.H., NEMERSON Y.;
 RL BIOCHEMISTRY 27:4227-4231(1988).
 CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF
 CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1
 CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND
 CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
 CC RESPONSE.
 DR EMBL; J02931; HSTFP.
 DR EMBL; M16553; HSTF1.
 DR EMBL; J02846; HSTFPB.
 DR PIR; A28320; KFHU3.
 DR PIR; A43645; A43645.
 DR MIM; 134390; TENTH EDITION.
 DR PROSITE; PS00621; TISSUE FACTOR.
 KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.
 FT SIGNAL 1 32
 FT CHAIN 33 295 TISSUE FACTOR.
 FT DOMAIN 33 251 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 252 274 POTENTIAL.
 FT DOMAIN 275 295 CYTOPLASMIC (POTENTIAL).
 FT SITE 46 48 WKS MOTIF.
 FT SITE 77 79 WKS MOTIF.
 FT SITE 190 192 WKS MOTIF.
 FT CARBOHYD 156 156 POTENTIAL.
 FT CARBOHYD 169 169 POTENTIAL.
 FT DISULFID 81 89
 FT DISULFID 218 241
 FT LIPID 277 277 PALMITATE.
 FT CONFLICT 260 260 V -> A (IN REF. 4).
 SQ SEQUENCE 295 AA; 33067 MW; 494480 CN;

Initial Score = 295 Optimized Score = 295 Significance = 61.80
 Residue Identity = 100% Matches = 295 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
      220     230     240     250     260     270     280

```

|||||
NSPLNVS
290 X

2. FURM-969863-FIG2.PEP (1-295)

TF_BOVIN TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF BOVIN STANDARD; PRT: 292 AA.
AC P30931;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=ADRENAL GLAND;
RM 92109720
RA TAKAYENOKI Y., MUTA T., MIYATA T., IWANAGA S.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 181:1145-1150(1991).
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DR EMBL: S74147; S74147.
DR PIR: J01319; KFB03.
KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.
FT SIGNAL 1 35
FT CHAIN 36 292 TISSUE FACTOR.
FT DOMAIN 36 248 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 249 271 POTENTIAL.
FT DOMAIN 272 292 CYTOPLASMIC (POTENTIAL).
FT SITE 46 48 WKS MOTIF.
FT CARBOHYD 43 43 POTENTIAL.
FT CARBOHYD 153 153 POTENTIAL.
FT CARBOHYD 181 181 POTENTIAL.
FT DISULFID 81 89 BY SIMILARITY.
FT DISULFID 215 238 BY SIMILARITY.
FT LIPID 274 274 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 292 AA; 32475 MW; 478152 CN;

Initial Score = 148 Optimized Score = 257 Significance = 46.15
Residue Identity = 69% Matches = 204 Mismatches = 71
Gaps = 3 Conservative Substitutions = 17

X 10 20 30 40 50 60 70
METPAWPRVPRPETAVARTLLGLWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
MATPNCPRVPCPAAVARALLFGLVLIGGAGVAGTTDVVAYNITWKSTNFKTILEWEPKPINHVYTVQISP
X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVSTGSAGEPLYENSPEFTPYLETNLGQPT
RLGNWKNKCFYTTNTECDVTDEIVKNVRETYLARVLSYPA---DTSSSTVEPPFTNSPEFTPYLETNLGQPT
80 90 100 110 120 130 140

150 160 170 180 190 200 210
IQSFEQVGTQVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLVYWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEQVGTQVNVTVQDARTLVANSALFLSLRDVFGKDLNYTLVYWKASSTGKKKATTNTNGFLIDVDKGEN
150 160 170 180 190 200 210

220 230 240 250 260 270 280
YCFSVQAVIPSRTVNRKSTDSPECMGQEGEFREIFYIIGAVVFVVIILVILAIHLKCRKAGVGQSWKE
YCFHVQAVILSRVNGKSPESPIKTSHEKVLSTELFFIIGTVMLVIIIFIVVLSVSLHKCRKVRERSGKE
220 230 240 250 260 270 280

290 X
NSPLNVS
|||||
NTPLNAA
290 X

3. FURM-969863-FIG2.PEP (1-295)

TF_RABIT TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF RABIT STANDARD; PRT: 292 AA.
AC P24055;
DT 01-MAR-1992 (REL. 21, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).
 OS DRYCTOLAGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; LAGOMORPHA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RM 91200676
 RA ANDREWS B.S., REHENTULLA A., FOWLER B.J., EDGINGTON T.S., MACKMAN N.;
 RL GENE 98:265-269(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RM 92081032
 RA PAWASHE A., EZEKOWITZ M., LIN T.C., HORTON R., BACH R., KONIGSBERG W.;
 RL THROMB. HAEMOST. 66:315-320(1991).
 CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -!- TISSUE SPECIFICITY: BRAIN, HEART.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 DR EMBL; M55390; OCRF.
 DR PIR; JU0441; KFRB3.
 DR PROSITE; PS00621; TISSUE FACTOR.
 KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.
 FT SIGNAL 1 32
 FT CHAIN 33 292 TISSUE FACTOR.
 FT DOMAIN 33 250 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 250 271 POTENTIAL.
 FT DOMAIN 272 292 CYTOPLASMIC (POTENTIAL).
 FT SITE 44 46 WKS MOTIF.
 FT SITE 75 77 WKS MOTIF.
 FT CARBOHYD 41 41 POTENTIAL.
 FT CARBOHYD 114 114 POTENTIAL.
 FT CARBOHYD 154 154 POTENTIAL.
 FT CARBOHYD 167 167 POTENTIAL.
 FT CARBOHYD 182 182 POTENTIAL.
 FT DISULFID 79 87 BY SIMILARITY.
 FT DISULFID 216 239 BY SIMILARITY.
 FT LIPID 274 274 PALMITATE (BY SIMILARITY).
 SQ SEQUENCE 292 AA; 32738 MW; 459706 CN;

Initial Score = 209 Optimized Score = 254 Significance = 44.91
 Residue Identity = 69% Matches = 206 Mismatches = 67
 Gaps = 3 Conservative Substitutions = 19

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLGLWVFAQVAGASGTNTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
MAPPTRLQVPRPGTAVPYTVLLGLWLLAQVARAADTTGR--AYNLTKWSTNFKTILEWEPKSIDHVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNGLGPT
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RLENWKSCKFLTAETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEPPFRNSPEFTPYLDTNGLGPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKNVTVEDERTLVRNNTFLSLRDVFGKDLIYTYLWYKSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEQVGTKNVTVQDARTLVRNNGTFLSLRAVFGKDLNYTYLWYRASSTGKKTATTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRITVNRKSTDSPECMGQEKGEFREIFYIIGAVVFVVIILVILAILSHKCRKAGVGQSWKE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
YCFSVQAVIPSRKRKQSRPESLTETSREOGRAREMFFIIGAVV-VVALLIIVLSVTVYKCRKARAGPSCKE
      220     230     240     250     260     270     280

290 X
NSPLNVS
||||:
SSPLNIA
290 X
  
```

4. FURM-969863-FIG2.PEP (1-295) TF_MOUSE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF_MOUSE STANDARD; PRT; 294 AA.
 AC P20352;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)

GN CF-3.
 OS MUS MUSCULUS (MOUSE).
 DC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 DC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 91093171
 RA RANGANATHAN G., BLATTI S.P., SUBRAMANIAM M., FASS D.N., MAIHLE N.J.,
 RA GETZ M.J.;
 RL J. BIOL. CHEM. 266:496-501(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RM 89343974
 RA HARTZELL S., RYDER K., LANAHAN A., LAU L.F., NATHANS D.;
 RL MOL. CELL. BIOL. 9:2567-2573(1989).
 CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 DR EMBL; M57896; MMTFA.
 DR EMBL; M26071; MMTF.
 DR PIR; A32318; KFM53.
 DR PROSITE; PS00621; TISSUE FACTOR.
 KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.
 FT SIGNAL 1 28
 FT CHAIN 29 294 TISSUE FACTOR.
 FT DOMAIN 29 251 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 252 274 POTENTIAL.
 FT DOMAIN 275 294 CYTOPLASMIC (POTENTIAL).
 FT SITE 245 247 WKS MOTIF.
 FT CARBOHYD 37 37 POTENTIAL.
 FT CARBOHYD 57 57 POTENTIAL.
 FT CARBOHYD 169 169 POTENTIAL.
 FT CARBOHYD 200 200 POTENTIAL.
 FT DISULFID 75 83 BY SIMILARITY.
 FT DISULFID 218 241 BY SIMILARITY.
 FT LIPID 275 275 PALMITATE (BY SIMILARITY).
 FT CONFLICT 26 26 I -> T (IN REF. 2).
 SQ SEQUENCE 294 AA; 32935 MW; 468130 CN;

Initial Score = 87 Optimized Score = 219 Significance = 30.49
 Residue Identity = 52% Matches = 158 Mismatches = 114
 Gaps = 13 Conservative Substitutions = 16

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|      |      |      |      |      |      |      |      |      |      |      |
MAILVRPRL---AALAPT-FLGCLLLQVIAGAGIPEK--AFNLTWISTDFKTILEWQPKPTNYTYTVQISD
X      10      20      30      40      50      60

      80      90     100     110     120     130
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYP-AGNVESTGS-----AGEPLYENSPEFTPYLET
:      |      |      |      |      |      |      |      |      |      |      |
RSRNWKNKCFSTTDTTECDLTDEIVKDVTVWAYEAKVLSVPRRNSVHGDGDLVIHGEEPPFTNAPKFLPYRDT
70      80      90     100     110     120     130

140     150     160     170     180     190     200     210
NLGQPTIQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTYLWKSSSSGKKTAKTNTNEFLID
|      |      |      |      |      |      |      |      |      |      |
NLGQPVIIQFEQDGRKLNVVVKDSLTLVRKNGFTLTLRQVFGKDLGYIITYRKGSSTGKKTNIITNNEFSID
140     150     160     170     180     190     200     210

      220     230     240     250     260     270     280
VDKGENYCFVSQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGV
:      |      |      |      |      |      |      |      |      |      |
VEEGVSYCFVQAMIFSRKTNQNSPGSSTVCTEQWKSFLGETLIIVGAVVLLATIFIILSLCKRRKNRA
      220     230     240     250     260     270     280

      290 X
GQSWKENSPLNVS
|      |      |
GQKGG-NTPSRLA
      290 X
  
```

5. FURM-969863-FIG2.PEP (1-295)
 VGLF_NDVQ FUSION GLYCOPROTEIN PRECURSOR (CONTAINS: FUSION GL

ID VGLF_NDVQ STANDARD; PRT: 553 AA.
 AC P33615;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE FUSION GLYCOPROTEIN PRECURSOR (CONTAINS: FUSION GLYCOPROTEINS F1 AND

XX
FH Key Location/Qualifiers
FH
FT sig_peptide 64..144
FT source 1..1683
FT /strain="Sprague-Dawley"
FT /organism="Rattus norvegicus"
FT /cell_type="aortic smooth muscle"
FT CDS 64..951
FT /note="NCBI gi: 464011"
FT /product="tissue factor protein"
FT /codon_start=1
XX
SQ Sequence 1683 BP; 473 A; 379 C; 379 G; 452 T; 0 other;

Initial Score = 321 Optimized Score = 555 Significance = 21.64
Residue Identity = 60% Matches = 600 Mismatches = 321
Gaps = 69 Conservative Substitutions = 0

```

      10      20      30      40      50      60      70
CTGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCCACGGAACCC
      |      |      |      |      |      |      |
      X      10      20      30
      80      90      100     110     120     130     140
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCC-CCGAGACCGC
      |      |      |      |      |      |      |
      40      50      60      70      80      90
CCGCGACCTCGCCAGCAGCCCTTGACATGGCTATCCC--CATG---CG---CCCGCGCTCTAG-CGGC
      |      |      |      |      |      |      |
      100     110     120     130     140     150     160
CGTCGCTCGGACGCTCTGCTCGGTGGTCTTCGCC--CAGGTGGCCGGCGCTTCAGGCA---CTACAAAT
      |      |      |      |      |      |      |
      170     180     190     200     210     220     230
AAAG-CGTTTAACTTGAATATCACTGATTCAAGACAATCTTGGAGTGGCAACCGAAACCCACCAA
      |      |      |      |      |      |      |
      240     250     260     270     280     290     300
GTCATCAAGTCTACACTGTTCAAATA-AGCACTA-AGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAA
      |      |      |      |      |      |      |
      310     320     330     340     350
CTATACCTACACTGTTTCAATAAGCGATAGATCTAGAACTGGA-AATACAAATGCA---CTGGAACCACA
      |      |      |      |      |      |      |
      360     370     380     390     400
CAGACACAGAGTG---TGACCTACCGA---CGA-GATTGTGAA--GGA--TGTAAGCA---GACGTA-CT
      |      |      |      |      |      |      |
      410     420     430     440     450     460     470
-TGGCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGA-GCACCGTCTGCTGGGGAG---CCTCTGTA
      |      |      |      |      |      |      |
      480     490     500     510     520     530     540
TGAGAACTCCCAG-AGTTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTGAAC
      |      |      |      |      |      |      |
      550     560     570     580     590     600     610
AGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAA
      |      |      |      |      |      |      |
      620     630     640     650     660     670     680
GCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGA
      |      |      |      |      |      |      |
      690     700     710     720     730     740     750
AAACAGCCAAACAAACACTAATGAGTTTTGATTGATGTGGATAAAGGAGAAACTACTGTTTCAGTGTTC
      |      |      |      |      |      |      |
      760     770     780     790     800     810     820
AAGCGGTACGAACTGAAGGTGACTGTAAAGACTCATTACATTAGTCAGAAAGAATGGTACATTCCTCA
      |      |      |      |      |      |      |
      830
AAGCAGTGATTCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTA-TGGGCCAGGAG
```

```

|TCCCATGGAGGAAC-CAAC---TCATGGAAAGGAAACACTCTTTGGAACATCATGGGAGGAACCGCCAT-
380      390      400      410      420      430      440

480      490      500      510      520      530      540
TGAGAACTCCCCAG-AGTTACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTGAGATTTTGAAC
TTACAAATGCCCGGAAGTTTTTACCTTACCGAGATACAAAAATTGGACAGCCAGTAATTGAGAAGTATGAAC
450      460      470      480      490      500      510

550      560      570      580      590      600      610
AGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAA
AAGGCGGTACGAACTGAAGGTGACTGTAAAAGACTCATTACATTAGTCAGAAAGAATGGTACATTCTCA
520      530      540      550      560      570      580

620      630      640      650      660      670      680      690
GCCTCCGGGATGTTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGA
CTCTGCGGCAAGTTTTTGGCAATGACTTGGGTATATTCTTACGTATCGGAAAGACTCAAGCACAGGAAGGA
590      600      610      620      630      640      650

700      710      720      730      740      750      760
AAACAGCCAAACAAACACTAATGAGTTTTTGAATTGATGTGGATAAAGGAGAAACTACTGTTTCAGTGTTC
AAACAAACACTACACATACCAATGAATCTTGAATTGATGTGGAAAAGGGGTAAGCTACTGCTTCTTCGCAC
660      670      680      690      700      710      720      730

770      780      790      800      810      820      830
AAGCAGTGATTCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTA-TGGGCCAGGAG
AAGCCGTGATTTTCTCCAGGAAACTAACCACAAGAGCCAGAAAGCATCACCAGTGCAGTGAAGCAATG-G
740      750      760      770      780      790      800

840      850      860      870      880      890      900
AAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTTTGGTTCATCATCCTTGTATCATC
AAGAGTGTCTGGGAGAAACACTCATCTTGTGGGAGCAGTGGTCTTCTGGTCACTGTCTTTATCATCCTG
810      820      830      840      850      860      870

910      920      930      940      950      960      970
CTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAAT
CTGACCATATCTCTGTGCAAGCGCAGAAAGAACAGAGCAGGACAGAAAGGA---AGAACACCCCGTGGCGC
880      890      900      910      920      930      940

980      X
GTTTCATAA
TTGGCATAGACGAGGAGGCTGACGCTGCTGACTGTCACTGCCACACGGCACTGTTA
950      960      970      980      990      1000

```

11. FURM-969863-FIG2.SEQ (1-987)

RN07619 Rattus norvegicus Sprague-Dawley tissue factor pro

ID RN07619 standard; RNA; ROD; 1683 BP.

XX
AC U07619;

XX
DT 25-MAR-1994 (Rel. 39, Created)
DT 25-MAR-1994 (Rel. 39, Last updated, Version 1)

XX
DE Rattus norvegicus Sprague-Dawley tissue factor protein mRNA,
DE complete cds.

XX
KW .

XX
OS Rattus norvegicus (rat)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

XX
RN [1]
RP 1-1683
RA Rosenfield C., Guha A., Nemerson Y., Taubman M.B.;
RT "Rat tissue factor: its protein sequence and clotting properties
RT are divergent from that of the mouse";
RL Unpublished.

XX
RN [2]
RP 1-1683
RA Rosenfield C.;
RT ;
RL Submitted (09-MAR-1994) to the EMBL/GenBank/DBJ databases.
RL Claire-Lise Rosenfield, Medicine, Mount Sinai School of Medicine,
RL One Gustave L. Levy Place, New York, NY 10029, USA

XX
CC NCBI oi: 464010

10. FURM-969863-FIG2.SEQ (1-987)

RRU07619 Rattus norvegicus Sprague-Dawley tissue factor pro

LOCUS RRU07619 1683 bp mRNA ROD 25-MAR-1994
 DEFINITION Rattus norvegicus Sprague-Dawley tissue factor protein mRNA,
 complete cds.
 ACCESSION U07619
 KEYWORDS .
 SOURCE rat
 ORGANISM Rattus norvegicus
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
 Eutheria; Rodentia; Myomorpha; Muridae; Rattus.
 REFERENCE 1 (bases 1 to 1683)
 AUTHORS Rosenfield,C., Guha,A., Nemerson,Y. and Taubman,M.B.
 TITLE Rat tissue factor: its protein sequence and clotting properties are
 divergent from that of the mouse
 JOURNAL Unpublished
 STANDARD full automatic
 REFERENCE 2 (bases 1 to 1683)
 AUTHORS Rosenfield,C.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-1994) Claire-Lise Rosenfield, Medicine, Mount
 Sinai School of Medicine, One Gustave L. Levy Place, New York, NY
 10029, USA
 STANDARD full automatic
 COMMENT NCBI gi: 464010
 FEATURES
 Location/Qualifiers
 sig_peptide 64..144
 source 1..1683
 /strain="Sprague-Dawley"
 /organism="Rattus norvegicus"
 /cell type="aortic smooth muscle"
 CDS 64..951
 /note="NCBI gi: 464011"
 /product="tissue factor protein"
 /codon start=1
 /translation="MAIPMRPRLAALAPTFLGFLLLQVAVGAGTPPCKAFNLTWIST
 DFKTILEWQPKPTNYTYTVQISDRSRNWKYKCTGTTDTECDLTDEIVKDVNWTYEARV
 LSPVWRNSTHGKETLFGTHGEPPFTNARKFLPYRDTKIGQPVIGKYEQGGTKLKVTV
 KDSFTLVRKNGFTLRLQVFGNDLGYILTyrKDSSTGRKNTNTHNEFLIDVEKGVSY
 CFFAQAIVFSRKTNHKSPESTKCTEQWKSVLGETLIIVGAVVFLVTVFIILLTISLC
 KRRKNRAGQKRKNTPSRLA"
 BASE COUNT 473 a 379 c 379 g 452 t
 ORIGIN

Initial Score = 321 Optimized Score = 555 Significance = 21.64
 Residue Identity = 60% Matches = 600 Mismatches = 321
 Gaps = 69 Conservative Substitutions = 0

```

      10      20      30      40      50      60      70
CTGCACTCCCTCTGGCCGCCCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
      x      10      20      30
      80      90      100     110     120     130     140
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCCTGCCCGGGTCCCGCGCC-CCGAGACCGC
      40      50      60      70      80      90
CCGGACCTCGCCAGCAGCCCTTGACATGGCTATCCC--CATG---CG---CCCGCGCTCCTAG-CGGC
      150     160     170     180     190     200     210
CGTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCC--CAGGTGGCCGGCTTCAGGCA---CTACAAAT
      100     110     120     130     140     150     160
CCTCGCGCCAC-CT--TCTCGGCT--TCCTTCTCCTTCAGGTGGCCGTTGGTGCAGGCACTCCTCCAGGG
      220     230     240     250     260     270     280
ACTGTGGCAGCATATAATTAACTTGGAAATCAACTAATTCAAGACAATTTGGAGTGGGAACCCAAACCC
      170     180     190     200     210     220     230
AAAG-CGTTTAATTAACTTGGATATCAACTGATTCAAGACAATCTTGGAGTGGCAACCGAAACCCACCAA
      290     300     310     320     330     340     350
GTCAATCAAGTCTACACTGTTCAAATA-AGCACTA-AGTCAGGAGATTGGAAAAGCAAAATGCTTTTACACAA
      240     250     260     270     280     290     300
CTATACCTACACTGTTTCAATAAGCGATAGATCTAGAAACTGGA-AATACAAATGCA---CTGGAACACA
      360     370     380     390     400
CAGACACAGAGTG---TGACCTCACCGA---CGA-GATTGTGAA--GGA--TGTGAAGCA--GACGTA-CT
      310     320     330     340     350     360     370
GACACTGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGTGGACCTATGAAGCAAGGGTCTATCT
      410     420     430     440     450     460     470
-TGGACCGCTCTCTCTACCCGCGACGCAATGTGGAGA-CCACCGGTTCTGCTGGGAG---CTCTCTGA

```

50 60 70 80 90 100
 TCC-CCAGC---CCCACG-GGCGCCACGGAACCCGCTCGATCTCGCCGCAACTGGTAGACATGGAGACCC
 TCCTGTAGCGTAGCCAACGCGCCGCGCTGAAGCCCCGAGACCTCGCCTCCAGCCCTTGGACATGGCGATCC
 80 90 100 110 120 130 140
 110 120 130 140 150 160 170 180
 CTGCCTGGCCCGGGTCCCGCGCC-CCGAGACCGCGCTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCCGC
 --TCGTG---CG---CCCGCGCCTCCTAG-CGGCTCTCGCGCCACG---TTTCTCGGCTGCCTCCTCCTC
 150 160 170 180 190 200
 190 200 210 220 230 240 250
 CAGGTGGCCGCGCTTCAGGCACTACAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTC
 CAGGTGACCGCGGGTGCAGGCATTCCAGAGAAAG-CGTTTAAATTTAACTTGGATATCAACTGATTTCAGAC
 210 220 230 240 250 260 270
 260 270 280 290 300 310 320
 AAGACAATTTGGAGTGGGAACCCAAACCCGTCATCAAGTCTACACTGTTCAAATAA--GCACTA-AGTCA
 AATTTTGGAGTGGCAACCCAAACCCCAACTATACCTACACTGTACAGAT-AAGTGATCGATCTAGAAACT
 280 290 300 310 320 330 340
 330 340 350 360 370 380
 GGAGATTGGAAGCAATGCTTTTACACAACAGACACAGAGTGTGACCTCA-CCGA---CG---AGATTGT
 GGAA--AACAAG-TGCTTCTCGACCAC-AGACACCGAGTGGCAGCTCACAGACGAGATCGTGAAGGATGT
 350 360 370 380 390 400 410
 390 400 410 420 430 440
 GA--AGG--ATGTGAAGCAGACGTACT---TG--GCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGAG
 GACCTGGGCCTATGAAGCAAAGTCTCTCTGTCCACGGAGGAAGT---CAGTTCATGG-AGACGGAGAC
 420 430 440 450 460 470
 450 460 470 480 490 500 510
 CACC---GGTTC-TGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAAC
 CAACTTGTGATTCATGGGAGGAGCGCCATTTACAAACGCCCAAGTTTTTACCTTACCGAGACACAAAC
 480 490 500 510 520 530 540 550
 520 530 540 550 560 570 580
 CTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAGAAGTGAACGG
 CTTGGACAGCCAGTAATTCAGCAGTTTGAACAAGATGGTAGAAAAGTGAACGTGGTTGTAAGAACTCACTT
 560 570 580 590 600 610 620
 590 600 610 620 630 640 650 660
 ACTTTAGTCAGAAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAATTTATACACTT
 ACATTAGTCAGAAAGATGGTACATTCCTCACCCTGCGGCAAGTCTTTGGCAAGGACTTGGGTATATAATT
 630 640 650 660 670 680 690
 670 680 690 700 710 720 730
 TATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTTTGATTGATGTG
 ACTTATCGGAAAGGCTCAAGCACGGGAAGAAAACAAACATTACAAACACCAATGAATTCTCGATTGATGTG
 700 710 720 730 740 750 760
 740 750 760 770 780 790 800
 GATAAAGGAGAACTACTGTTTCAAGTGTCAAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACA
 GAAGAAGGAGTAAGCTACTGCTTTTTTGTACAAGCTATGATTTTCTCCAGGAAAACCTAACCAAAATAGCCCA
 770 780 790 800 810 820 830
 810 820 830 840 850 860 870
 GACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGG--GAATT--CAG--AGAAATATTCTACATCATTGGA
 GGAAG--CAGTACAGTG--TGACC--GAGCAATGGAAGAGTTTCTGGGAGAAACACTCATCATTTGTGGGA
 840 850 860 870 880 890 900
 880 890 900 910 920 930 940
 GCTGTGGTATTTGTGGTCATCATCTTGTATCATCTTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGA
 GCAGTGGTGCTCCTGGCCACCATCTTTATCATCTCTGTCCATATCTCTGTGCAAGCGCAGAAAGAACCGGA
 910 920 930 940 950 960 970
 950 960 970 980 X
 GTGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
 GCGGGACAGAAAGGGA---AGAACACCCCGTGGCGCTGGCATAGAGGAAAGGCTGAAGCGCTAACGCTCAC
 980 990 1000 1010 1020 1030 1040
 ACTGCCTGCACGGCACTGTTGCG
 1050 1060

```

570      580      590      600      610      620      630
GAATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTT
500      510      520      530      540      550      560      570
GAACGTGGTTGTAAGAACTCACTTACATTAGTCAGAAAGAAATGGTACATTCCTCACCCTGCGGCAAGTCTT

640      650      660      670      680      690      700
TGGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAA
580      590      600      610      620      630      640
TGGCAAGGACTTGGGTTATATAATTAATTTATCGGAAAGGCTCAAGCACGGGAAAGAAAACAAACATTACAAA

710      720      730      740      750      760      770
CACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAACTACTGTTTCAGTGTCAAGCAGTGATTCCCTC
650      660      670      680      690      700      710
CACCAATGAATTCCTGATTGATGTGGAAGAAGGAGTAAGCTACTGCTTTTTTGTACAAGCTATGATTTTCTC

780      790      800      810      820      830      840
CCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGG--GAATT--CA
720      730      740      750      760      770      780
CAGGAAACTTAACCAAAATAGCCAGGAAG--CAGTACAGTG--TGCACC--GAGCAATGGAAGAGTTTCCT

850      860      870      880      890      900      910
G--AGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATC
790      800      810      820      830      840      850
GGGAGAAACACTCATCATTTGTGGGAGCAGTGGTGCTCTGGCCACCATCTTTATCATCCTCTGTCCATATC

920      930      940      950      960      970      980      X
TCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTCATAA
860      870      880      890      900      910      920
TCTGTGCAAGCGCAGAAAGAACCGAGCGGGACAGAAAGGGA---AGAACACCCCGTGGCGCTGGCATAGAG

GAAAGCGTGAAGCGCTAACGCTCACACTGCCTGCACGGCACTGTTGCG
930      940      950      960

```

9. FURM-969863-FIG2.SEQ (1-987)

MUSTF Mouse tissue factor (mtf) mRNA, complete cds.

```

LOCUS      MUSTF      1821 bp ss-mRNA      ROD      15-DEC-1989
DEFINITION Mouse tissue factor (mtf) mRNA, complete cds.
ACCESSION  M26071
KEYWORDS   membrane-bound glycoprotein; tissue factor.
SOURCE      Mouse (strain BALB/c) fibroblast 3T3 cell line, cDNA to mRNA, and
            DNA (bp 1-41), clone 3CH 482.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 1821)
AUTHORS     Hartzell,S., Ryder,K., Lanahan,A.A., Lau,L.F. and Nathans,D.
TITLE        A growth factor-responsive gene of murine BALB/c 3T3 cells encodes
            a protein homologous to human tissue factor
JOURNAL      Mol. Cell. Biol. 9, 2567-2573 (1989)
STANDARD     full automatic
COMMENT      Draft entry and computer-readable sequence for [1] kindly submitted
            by S.Hartzell, 12-JUL-1989.
            NCBI gi: 201924
FEATURES
  mRNA       Location/Qualifiers
            29..1821
            /note="TFP mRNA"
  CDS        135..1019
            /note="tissue factor protein; NCBI gi: 201925."
            /codon start=1
            /translation="MAILVRPRLAALAPTFLGCLLLQVTAGAGIPEKAFNLTWISTD
            FKTILEHQPKNYTYTVQISDRSRNWNKCFSTTDECDLTDEIVKDVWYAEAKVL
            SVPRRNSVHGDGDQGLVIHGEPPFTNAPKFLPYRDTNLGQPVIQFEQDGRKLNVVVK
            DSLTLVRKNGFTLRLQVFGKDLGYIITYRKGSSGTGKTNITNTEFSIDVEEGVSYC
            FFVQAMIFSRKTQNSPGSSTVCTEQWKSFLGETLIIVGAVVLLATIFIILLSISLCK
            RRKNRAGGKGKNTPSRLA"
  source     1..1821
            /organism="Mus musculus"
BASE COUNT  516 a      415 c      412 g      478 t
ORIGIN      Unreported

```

Initial Score = 343 Optimized Score = 582 Significance = 23.29
 Residue Identity = 61% Matches = 632 Mismatches = 321
 Gaps = 77 Conservative Substitutions = 0

```

X      10      20      30      40
CTCGCA--CTCCCTCTGGCCGG--CCCAGGGCGC-CTTCAGCCCAAC-C
TTTATAACGCACCCCGCGGACCCCGGCAGCCTGGGTACAGCCGGTACCCATCACTCGCTCCCTCCGATCGC
10      20      30      40      50      60      70

```

8. FURM-969863-FIG2.SEQ (1-987)

MUSTFA Mouse tissue factor mRNA, complete cds.

LOCUS MUSTFA 1262 bp ss-mRNA ROD 23-JAN-1991
DEFINITION Mouse tissue factor mRNA, complete cds.
ACCESSION M57896 J05713
KEYWORDS tissue factor.
SOURCE Mouse (strain AKR) embryo fibroblast, cDNA to mRNA, clone c70.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 1262)
AUTHORS Ranganathan,G., Blatti,S.P., Subramanian,M., Fass,D.N., Maihle,N.J.
and Getz,M.J.
TITLE Cloning of murine tissue factor and regulation of gene expression
by transforming growth factor type beta-1
J. Biol. Chem. 266, 496-501 (1991)
JOURNAL full automatic
STANDARD NCBI gi: 201926
COMMENT
FEATURES
CDS Location/Qualifiers
35..919
/note="NCBI gi: 201927"
/product="tissue factor"
/codon start=1
/translation="MAILVRPRLAALAPTFLGCLLLQVIAGAGIPEKAFNLTWISTD
FKTILEWQPKPTNYTYTVQISDRSRNWKNCFSITDTECDLTDEIVKDVWYAEAKVL
SVPRRNSVHGDDQLVIHGEEPPFTNAPKFLPYRDTNLGQPVIGQDGRKLNVVVK
DSLTLVRKNGTFLTRQVFGKDLGYIITYRKGSSGTGKKTNITNTEFSIDVEEGVSYC
FFVQAMIFSRKTNQNSPGSSVCTEQWKSFLGETLIIVGAVLLATIFIILLSISLCK
RRKNRAGQKGNTPSRLA"
source 1..1262
/organism="Mus musculus"
BASE COUNT 358 a 317 c 305 g 282 t
ORIGIN

Initial Score = 344 Optimized Score = 549 Significance = 23.36
Residue Identity = 62% Matches = 593 Mismatches = 292
Gaps = 71 Conservative Substitutions = 0

```

      20      30      40      50      60      70      80
GCCGGCCAGGGCGCCTTCAGCCCAACCTCCCAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGC
                                     TGAAGCCCCGAGACCTCGCCTC
                                     X          10          20

      90     100     110     120     130     140     150
CAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCC-CCGAGACCGCGCTCGCTCGGACGCT
CAGCCCTTGGACATGGCGATCC--TCGTG---CG---CCCGCGCTCCTAG-CGGCTCTCGCGCCACG--
      30      40      50      60      70      80

    160     170     180     190     200     210     220     230
CCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATT
-TTCTCGGCTGCCTCCTCCTCAGGTGATCGCGGTGCAGGCATTCCAGAGAAAC-CGTTTAATTTAACTT
      90     100     110     120     130     140     150

    240     250     260     270     280     290
AACTTGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAAC--CCGTCAAT--CAAGTCTACA
GGATATCAACTGATTCAAGACA----ATTTGGAGTGGCAACCCAAACCCACCAACTATACCTACACTGTA
      160     170     180     190     200     210     220

    300     310     320     330     340     350     360
CTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCA--AATGCTTTTACACAACAGACACAGAGTGTGA
CAGAT-AAGTGATC--GATCTAGAACTGGAAGAAACAAGTGCTTCTCGACCAC-AGACACCGAGTGCGACC
      230     240     250     260     270     280

    370     380     390     400     410     420
CCTCA-CCGA---CG---AGATTGTGA--AGG--ATGTGAAGCAGACGTACT---TG--GCACGGGTCTTCT
TCACAGACGAGATCGTGAAGGATGTGACCTGGGCCTATGAAGCAAAGGTCTCTGTCCACGGAGGAACT
      290     300     310     320     330     340     350

    430     440     450     460     470     480     490
CCTACCCGGCAGGGAATGTGGAGAGCACC---GGTTC-TGCTGGGAGCCTCTGTATGAGAACTCCCAGA
CAGTTATG--GGGA---CGGAGACCAACTTGTGATTCATGGGAGGAGCCGCAATTTACAAACGCCCCAA
      360     370     380     390     400     410     420

    500     510     520     530     540     550     560
GTTACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGT
GTTTTTACCTTACCGAGACACAAACCTCGGACAGCCAGTAATTCAGCAGTTTGAACAAGATGGTAGAAAAT
      430     440     450     460     470     480     490
```

CAGGGCGCCTTACGCCCAACCTCCCGAGCCCCACGGGCGCCACGGGAACCCGCTCGATCTCGCCGCCAACTGG
 850 860 870 880 890 900 910
 TAGACATGGAGACCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGTCCGCTCGGACGCTCCTGCTCG
 100 110 120 130 140 150 160
 TAGACATGGAGACCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGTCCGCTCGGACGCTCCTGCTCG
 920 930 940 950 960 970 980
 GCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGG-CACT-ACA-AATACTGTGGCAGCATATAATTTAACTT
 170 180 190 200 210 220 230
 GCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGTGAGTGGCACCAGCCCTGGAAGCCCGGGGCGCGCC--
 990 1000 1010 1020 1030 1040 1050
 GGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAAC--CCAAACCC--GTCAATCAAGTCTACACTGTT
 240 250 260 270 280 290 300
 --ACACGCAGGAGGGAGGCGACAGTCTTGG-CTGGCAGCGGGCTCGCCCTGGTTCCCGGGGCGCCCATGTT
 1060 1070 1080 1090 1100 1110 1120
 CAAATAAGC-ACTAAGTCAGGAGATTG-GAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGAC-CTC
 310 320 330 340 350 360 370
 GTCCCCCGCGCTACGGGACTCGGCTGCGCTCACCAGCCCGGCTTGA-ATGA--ACCGAGTCCGTGCGGC
 1130 1140 1150 1160 1170 1180 1190
 ACCGACGAGATTGTGAAGGATGTGAAGCAGACGTAAGTGGCAGGGTCTTCTCCTACC-CGGCAGGGAAT--
 380 390 400 410 420 430 440
 GCCCGCGGGAGT-TGCAGGGAG-GGAGTTGGCGCCCGAGACCCCG--CTGCCCTTCCGCTGGAGAGTTTGT
 1200 1210 1220 1230 1240 1250 1260
 GTGGAGAGCACCG-GTTCTGCTGGGAGCCTCTG--TATGAGAACTCCCGAGAGTTCACACCTTA--CCTGG
 450 460 470 480 490 500
 CTGCGGGTGTCCGAGTAAT--TGGACTGTTGTGCATAAGCGGACT---TTTAGCTCCCGCTTAACTCTGG
 1270 1280 1290 1300 1310 1320 1330
 AGACAAACCT---CGGACAG--CCAACAATTGAGAGTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGT
 510 520 530 540 550 560 570
 GGAAAGGGCTTCCAGTGAGTTGCGACCTCAATATGATAGGACTTGTGCTGCGTCTGCACGTGTTGGCGT
 1340 1350 1360 1370 1380 1390 1400
 AGAAGATGAACGGA-----CTTTAGTCAGAAG-GAA-CAACACTT--TCCTAAGCCTCCGGGATGTTTT--
 580 590 600 610 620 630
 -GCAGAGGTTTGGATATTATCTTTTATTATGTGCATCTTCCCTTAATAAGAGCGTCCCTGGTCTTTTCC
 1410 1420 1430 1440 1450 1460 1470
 TGGCAAGGACTTAATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAA--CA
 640 650 660 670 680 690 700
 TGGCCA--TCTT-TGTTCTAGGTTTGGGTAGAGGCAATCCAAAAGGGCTGGATTG----CTGCTTAGATTGG
 1480 1490 1500 1510 1520 1530
 AACACTAATGAGTTTTTGTATGATGGATAAAGGAGAAACTACTGTTTCAGTGTTCAGCAGTGATTCCC
 710 720 730 740 750 760 770
 AGCAGGTACAACGTTGTGATGCCCCGTATTTCTACGAGGTGTTT-GGGACGGCTAGAGACTGGGA---CC
 1540 1550 1560 1570 1580 1590 1600
 TCCCGAACAGTTAACCAGAGAGTACAGACAGCC---CGGTAGAGTGTATGGCCAGGAGAAAGGGGAATTC
 780 790 800 810 820 830 840
 TGCTG---CGT--ACTGGCAAG--CAGACCTTCATAAGAAATAAT-CCTGATCCA--ATACAGCCGA---C
 1610 1620 1630 1640 1650 1660
 AGAGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTATCATCCTGGCTATATCT
 850 860 870 880 890 900 910
 GGTGTGACAGGCCACA-CGTCCCCG-TG-GGTCTCTGTGG-----AAGTTT-----CAGTGTAGCGACATTT
 1670 1680 1690 1700 1710 1720
 C-TACACAAGTGTAGAAAGGCAGGAGTGG---GGCAGAGCTGGAAGGAG---AACTC---CCCAC-TG--
 920 930 940 950 960 970
 CAGATAAAAGTGGAAGGTAAGTTTGGCTTTTTTCATTGTATGCAGTCCTAACCTTGTGCACACGTGTG
 1730 1740 1750 1760 1770 1780 1790
 -----980 X
 ----AATGTTT---CATAA
 GGATTATCTTTTCCATAACTTACTGAAAACCCCTTCTGGCGGGCTGAACCTGACTCTTCTGAGCTGA
 1800 1810 1820 1830 1840 1850 1860

7. FURM-969863-FIG2.SEQ (1-987)

HUMTFPB Human tissue factor gene, complete cds.

LOCUS HUMTFPB 13865 bp ds-DNA PRI 15-JUN-1989
 DEFINITION Human tissue factor gene, complete cds.
 ACCESSION J02846
 KEYWORDS Alu repeat; cell surface integral membrane protein;
 cell surface receptor; tissue factor.
 SOURCE Human DNA, clones lambda-TF[559,679,753,885,1377].
 ORGANISM Homo sapiens
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
 REFERENCE 1 (bases 1 to 13865)
 AUTHORS Mackman,N., Morrissey,J.H., Fowler,B. and Edgington,T.S.
 TITLE Complete sequence of the human tissue factor gene, a highly
 regulated cellular receptor that initiates the coagulation protease
 cascade
 JOURNAL Biochemistry 28, 1755-1762 (1989)
 STANDARD full automatic
 COMMENT Draft entry and computer-readable sequence for [1] kindly provided
 by J.H.Morrissey, 25-OCT-1988.
 NCBI gi: 339505
 FEATURES
 Location/Qualifiers
 exon 922..1021
 /number=1
 /note="tissue factor"
 pri_m_transcript 799..13232
 /note="TF mRNA and introns"
 intron 1022..2189
 /note="TF intron A"
 exon 2190..2301
 /number=2
 intron 2302..6391
 /note="TF intron B"
 repeat_region 6127..6241
 /note="Alu repeat partial copy A"
 exon 6392..6591
 /number=3
 intron 6592..9288
 /note="TF intron C"
 repeat_region 8391..8677
 /note="Alu repeat copy B"
 exon 9289..9467
 /number=4
 intron 9468..10074
 /note="TF intron D"
 exon 10075..10234
 /number=5
 intron 10235..11954
 /note="TF intron E"
 repeat_region 10954..11249
 /note="Alu repeat copy C"
 exon 11955..12091
 /number=6
 repeat_region 12458..12757
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 /gene="F3"
 /note="tissue factor; NCBI gi: 339506."
 /codon start=1
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 TWKSTNFKTILEWPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVQT
 YLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTV
 DERTLVRRNNTFLSLRDVFGKDLIYTLYYWSSSSGKKTAKTNTNEFLIDVDKGENYC
 FSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAI SLHK
 CRKAGVGGSWKENSPLNVS"
 source 1..13865
 /organism="Homo sapiens"
 BASE COUNT 3711 a 2955 c 3240 g 3959 t
 ORIGIN 1 bp upstream of EcoRI site; chromosome 1.

Initial Score = 378 Optimized Score = 516 Significance = 25.91
 Residue Identity = 56% Matches = 591 Mismatches = 340
 Gaps = 119 Conservative Substitutions = 0

X 10 20
 CTGCACTCCCTCTGGCCGGCC
 |||||
 TATAGCGCGCGGGGACCGGCTCCCAAGACTGCGAGCTCCCGCACCCCTCGCACTCCCTCTGGCCGGCC
 780 790 800 810 820 X 830 840

30 40 50 60 70 80 90

CGAGCTCCCAACAACTCTGGGCTCCCGCATCCCTCCCGTTTCATCCCGAGCCCA-GGTGCTCCAGCCC
 10 20 30 X 40 50 60 70
 40 50 60 70 80 90
 AACCTCCC--CAGCCCCAC-----GGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGGT
 AACCTCGCAGCATCTCTACCTCTCCAGCCTCCGGGCTCAGCGGAATTTTGGAGCCTCGCCGTCAGCTCCG
 80 90 100 110 120 130 140
 100 110 120 130 140 150 160
 AGACATGGAGACCCCTGCCTGGCCCGGGTCCCGCGCCCGAGACCGCCGTCGCTCGGACGCTCCTGCTCGG
 GGACATGGCGACCCCAACGGGCGCCGGTGCCCTGCCCCAGGCGGAGTCGCTCGGGCTCTTCTATTCCG
 150 160 170 180 190 200 210
 170 180 190 200 210 220 230
 CTGGGTCTTCGCCCAGGTGGCGGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACTTGGAA
 CTTAGTCCTCATCCAGGGGCGCGGAGTCGCGGCACTACAGATGTAGTGGTAGCATATAATATAACTTGGAA
 220 230 240 250 260 270 280
 240 250 260 270 280 290 300 310
 ATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCAATCAAGTCTACACTGTTCAAATAAG
 GTCAACTAATTTCAAGACCATTTTGGAGTGGGAACCCAAACCCATCAATCATGTCTACACTGTTTCAAGATAAG
 290 300 310 320 330 340 350
 320 330 340 350 360 370 380
 CACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGACCTCACCAGCAGAT
 CCCTAGATTAGGAACTGGAAAAACAAATGCTTTTACACAACAAACAGGAGTGTGATGTCACTGATGAGAT
 360 370 380 390 400 410 420 430
 390 400 410 420 430 440 450
 TGTGAAGGATGTGAAGCAGAGTACTTTGGCAGGGTCTTCTCCTACCCGGCAGGAATGTGGAGACACCGG
 TGTGAAAAATGTGAGAGAGACATATTTGGCAGAGTCTTCTCCTACCCCGCAGACACT-----ACCA---G
 440 450 460 470 480 490
 460 470 480 490 500 510 520
 TTCTGCTGGGAGCCTCTGTATGAGAACTCCCGAGAGTTCACACCTTACCTGGAGACAAACCTCGGACAGCC
 TTCCACAGTGGAGCCTCCGTTTACCAACTCCCGGAGTTCACACCTTACCTAGAGACAAACCTTGGACAGCC
 500 510 520 530 540 550 560
 530 540 550 560 570 580 590
 AACAAATTCAGAGTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCAG
 AACAAATTCAGAGTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAGAAGATGCACGTACGTTAGTCAG
 570 580 590 600 610 620 630
 600 610 620 630 640 650 660 670
 AAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGAA
 AGCGAACAGCGCATTCCTAAGCCTCCGGGATGTTTTGGCAAGGACTTGAATTACACACTTTATTACTGGAA
 640 650 660 670 680 690 700 710
 680 690 700 710 720 730 740
 ATCTTCAAGTTCAGGAAAGAAAACGCCAAACAACTAATGAGTTTTGATTGATGTGGATAAAGGAGA
 AGCTTCCAGTACAGGAAAGAAAAGGCCACGACAAACACTAATGGGTTTTTGAATTGATGTGGATAAAGGCGA
 720 730 740 750 760 770 780
 750 760 770 780 790 800 810
 AAACACTGTTTCAAGTTCAGGAGTATCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGT
 AAACACTGTTTCAAGTTCAGGAGTATCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGT
 790 800 810 820 830 840 850
 820 830 840 850 860 870 880
 AGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTGTGGT
 CAAGTGCCTAGCCACGAGAAAGTTCTGTCCACAGAACTTTCTTCATCATTGGCACAGTGTGCTGGTGTAT
 860 870 880 890 900 910 920
 890 900 910 920 930 940 950
 CATCATCCTTGTCTATCCTGGCTATATCTTACACAAGTGTAGAAAGGAGGAGTGGGCGAGAGCTGGAA
 CATCATCCTTGTCTATCCTGGCTATATCTTACACAAGTGTAGAAAGGAGGAGTGGGCGAGAGCTGGAA
 930 940 950 960 970 980 990
 960 970 980 X
 GGAGAACTCCCACTGAATGTTTCATAA
 GGAGAACACGCGCTCAACGCTGCATAAAAGATCCTGCTCTTGGAGCTTTCTGCCAACGCTGCAGAGCTCGT
 1000 1010 1020 1030 1040 1050 1060 1070

CAGCCAACAATTTCAGAGCTTTGAACAGGTGGGACAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTA
 450 460 470 480 490 500 510
 GTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTAT
 600 610 620 630 640 650 660
 GTCAGAAGGAATGGGACATTCCTAAGTCTCCGGGCTGTGTTGGCAAGGACTTGAATTACACGCTTTATTAC
 520 530 540 550 560 570 580
 TGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAACTAATGAGTTTTTATTGATGTGGATAAA
 670 680 690 700 710 720 730
 TGGAGAGCTTCGAGCACAGGAAAGAAAACAGCCACGACAAACACTAATGAGTTTTTATTGATGTGGATAAA
 590 600 610 620 630 640 650 660
 GGAGAAAACACTACTGTTTCAAGTTCAGGAAAGAAAACAGCCAAACAACTAATGAGTTTTTATTGATGTGGATAAA
 740 750 760 770 780 790 800 810
 GGAGAAAACACTACTGTTTCAAGTTCAGGAAAGAAAACAGCCAAACAACTAATGAGTTTTTATTGATGTGGATAAA
 670 680 690 700 710 720 730
 CCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTT
 820 830 840 850 860 870 880
 CTCACGGAGTGCACACAGCCGCGAGCAGGGCAGGGCCAGGGAGATGTTCTTCATCATTGGAGCAGTGGTGGTC
 740 750 760 770 780 790 800
 GTGGTCATCATCCTTG-TCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAG
 890 900 910 920 930 940 950
 GTGGCCCT-----CTTGATCATCGTCTGTCTGTGACCGTGTACAAGTGCAGAAAGGCAGGGCGGGGCCAG
 810 820 830 840 850 860 870
 CTGGAAGGAGAACTCCCACTGAATGTTTCATAA
 960 970 980 X
 CGGGAAGGAGAGCTCCCCCTGAACATCGCTGAAGGGAGCGCCGCGGGCGGTGCCGGCTGCTGCCAATGCT
 880 890 900 X 910 920 930 940
 GTGTTGCACTGT
 950

6. FURM-969863-FIG2.SEQ (1-987)

S74147 tissue factor [cattle, adrenal gland, mRNA, 1877 n

LOCUS S74147 1877 bp mRNA MAM 10-JUL-1992
 DEFINITION tissue factor [cattle, adrenal gland, mRNA, 1877 nt]
 ACCESSION S74147
 KEYWORDS .
 SOURCE cattle adrenal gland
 ORGANISM Bos sp.
 Unclassified.
 REFERENCE 1 (bases 1 to 1877)
 AUTHORS Takayenoki,Y., Nuta,T., Miyata,T. and Iwanaga,S.
 TITLE cDNA and amino acid sequences of bovine tissue factor
 JOURNAL Biochem. Biophys. Res. Commun. 181, 1145-1150 (1991)
 STANDARD full automatic
 COMMENT GenBank staff at the National Library of Medicine created this
 entry [NCBI gibbsq 74147] from the original journal article.
 This sequence comes from Fig.2.
 NCBI gi: 241438
 FEATURES
 CDS
 Location/Qualifiers
 148..1026
 /note="TF; This sequence comes from Fig.2."
 NCBI gi: 241439"
 /product="tissue factor"
 /codon start=1
 /translation="MATPNGPRVPCPQAAVARALLFGLVLIQAGVAGTTDVVVAYNI
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 YLARVLSYPADTSSSTVEPPFINSPEFTPYLETNLGQPTIQSFEQVGTGLNVTVQDAR
 TLVRANSFAFLSLRDVFGKDLNYTLYYWKAASSTGKKKATNTNGFLIDVDKGENYCFHV
 QAVILSRVRVWQSPESPIKCTSHEKVLSTELFFIIGTVMLVIIIFIVVLSVSLHKCRK
 VRAERSGKENTPLNAA"
 source
 1..1877
 /organism="Bos sp."
 /note="cattle"
 BASE COUNT 529 a 416 c 412 g 520 t
 ORIGIN
 Initial Score = 443 Optimized Score = 759 Significance = 30.78
 Residue Identity = 76% Matches = 770 Mismatches = 207
 Gaps = 26 Conservative Substitutions = 0

X 10 20 30
 CTCGCACCTCCCTCTGGCCGGCCAGGGCGCCCTTCAGCCC

LOCUS RABRTF 1753 bp ss-mRNA MAM 08-MAY-1991
 DEFINITION Rabbit tissue factor mRNA, complete cds.
 ACCESSION M55390
 KEYWORDS tissue factor.
 SOURCE Rabbit (strain New Zealand white) heart, cDNA to mRNA, clone pRTF1.
 ORGANISM *Oryctolagus cuniculus*
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
 Eutheria; Lagomorpha; Leporidae.
 REFERENCE 1 (bases 1 to 1753)
 AUTHORS Andrews,B.S., Rehmulla,A., Fowler,B.J., Edgington,T.S. and
 Mackman,N.
 TITLE Conservation of tissue fator primary sequence among three mammalian
 species
 JOURNAL Gene 98, 265-269 (1991)
 STANDARD full automatic
 COMMENT NCBI gi: 165696
 FEATURES

mRNA Location/Qualifiers
 1..1753
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 sig_peptide 28..123
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 /product="tissue factor"
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 CDS 28..906
 /note="NCBI gi: 165697"
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 /codon start=1
 /translation="MAPPTRLQVPRPGTAVPYTVLLGWLLAQVARAADTTGRAYNLTW
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 ARVLSYPARNGMTTGFPEEPFRNSPEFTPYLDTNLGOPTIQSFQVGTGLNVTQDA
 RTLVRNGTFLSLRAVFGKDLNYTLYWRASSTGKKTATTNTNEFLIDVDKGENYCFS
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 ARAGPSCKESSPLNIA"
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 /organism="Oryctolagus cuniculus"
 BASE COUNT 455 a 394 c 471 g 433 t
 ORIGIN

Initial Score = 560 Optimized Score = 693 Significance = 39.54
 Residue Identity = 76% Matches = 702 Mismatches = 203
 Gaps = 15 Conservative Substitutions = 0

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                                     ATCCGCAC-TCCTTGTGGGC--
                                     X          10

100     110     120     130     140     150     160
CTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCGCTCGCTCGGACGCTCCTG
CT-TTGGACATGGCGCCCCCGACCCGGCTCCAGGTCCCGCGTCCCGGGACCGCTGTTCTTATACGGTGCTG
20      30      40      50      60      70      80      90

170     180     190     200     210     220     230
CTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACT
CTCGGCTGGTGTCTGCCCAGGTGGCCCGCGCGCGAGACACTACAGGTA-----GAGCATATAATCTAACT
100     110     120     130     140     150

240     250     260     270     280     290     300
TGGAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCCAAACCCGTCATCAAGTCTACACTGTTCAA
TGGAAGTCAACGAATTTCAAGACAATTTCTGGAGTGGGAACCCAAATCCATCGATCATGTCTACACAGTTCAG
160     170     180     190     200     210     220

310     320     330     340     350     360     370
ATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAGAGTGTGACCTACCGAC
ATAAGCACTAGGCTAGAAACTGGAAGAGCAAAATGTTTCTTAACCGCGGAGACGGAGTGGCAGCTACCGAT
230     240     250     260     270     280     290     300

380     390     400     410     420     430     440     450
GAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGAGC
GAGGTGCTGAAGGACGTGGGGCAGACGTACATGGCGCGGTCTCTCCTACCCGGCAAGGAACGGAAACACC
310     320     330     340     350     360     370

460     470     480     490     500     510     520
ACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCTCGGA
ACGGGTTTCCCGAGGAGCCTCCCTTTAGAAACTCCCGGAGTTCACGCCGTACCTGGACACAAACCTCGGC
380     390     400     410     420     430     440

530     540     550     560     570     580     590

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exon /number=4
 490..650
 /number=5
 BASE COUNT 330 a 306 c 386 g 278 t
 ORIGIN

Initial Score = 561 Optimized Score = 608 Significance = 39.61
 Residue Identity = 77% Matches = 613 Mismatches = 169
 Gaps = 11 Conservative Substitutions = 0

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                                     GCAGACACTACAGGTA-----
                                     X          10

220      230      240      250      260      270      280
CAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCGTCAATC
GAGCATATAATCTAACTTGAAGTCAACGAATTTCAAGACAATTTCTGGAGTGGGAACCCAAATCCATCGATC
  20       30       40       50       60       70       80

290      300      310      320      330      340      350      360
AAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTACACAACAGACACAG
ATGCTCTACACAGTTCAGATAAGCACTAGGCTAGAAAAGTGAAGAGCAAAATGTTCTTAACCGCGGAGACGG
  90      100     110     120     130     140     150     160

370      380      390      400      410      420      430
AGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTAAGTGGCAGGGTCTTCTCTACCCGG
AGTGGCAGCTCACCGATGAGTCTGTGAAGGACGTGGGGCAGACGTAACATGGCGGGTCTCTCTACCCGG
  170     180     190     200     210     220     230

440      450      460      470      480      490      500
CAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTACC
CAAGGAACGGAAACACCACGGGGTTCCTCCGAGGAGCCTCCCTTTAGAAACTCCCGGAGTTCACGCCGTACC
  240     250     260     270     280     290     300

510      520      530      540      550      560      570
TGGAGACAAACCTCGGACAGCCAACAATTAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAG
TGGACACAAACCTCGGACAGCCAACAATTAGAGCTTTGAACAAGTGGGACAAACTGAATGTGACAGTCC
  310     320     330     340     350     360     370

580      590      600      610      620      630      640
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AGGATGCACGCACGCTGGTTCAGAAGGAATGGGACATTCCTAAGTCTCCGGGCTGTGTTTGCAAGGACTGA
  380     390     400     410     420     430     440

650      660      670      680      690      700      710      720
TTTATACACTTTATTATTGGAATCTTCAAGTTCAAGAAAGAAAACAGCCAAAACAACTAATGAGTTTT
ATTACACGCTTTATTACTGGAGAGCTTCGAGCACAGGAAAGAAAACAGCCACGACAAACACTAATGAGTTTT
  450     460     470     480     490     500     510     520

730      740      750      760      770      780      790
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TGATCGACGTGGATAAAGGAGAAAAGTACTGTTTTCAGTGTTCAGCAGTGATTCCCTCTCGGAAAAGGAAGC
  530     540     550     560     570     580     590

800      810      820      830      840      850      860
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AGAGAGAGCCCGAGAGCCTCACTGAGTGCACAGCCGCGAGCAGGGCAGGGCAGGGAGATGTTCTTCATCA
  600     610     620     630     640     650     660

870      880      890      900      910      920      930
TTGGAGCTGTGGTATTTGTGGTCATCATCCTTG-TCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAG
TTGGAGCAGTGGTGGTCTGGTCCCT-----CTTGATCATCTGCTGTCTGTGACCGTGTACAAGTGCAGAAAG
  670     680     690     700     710     720     730

940      950      960      970      980      X
GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
GCGAGGGCGGGGCCAGCGGGAAGGAGAGTCCCGCTGAACATCGCCTGAAGGAGCGCGCGGGGGGTGC
  740     750     760     770     780     X     790     800

CGGCTGCTGCCAATGCTGTGTGCACTGT
  810     820     830
  
```

440 450 460 470 480 490 500
 GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTACACCTTAC
 410 420 430 440 450 460 470 480
 GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTACACCTTAC
 510 520 530 540 550 560 570
 CTGGAGACAAACCTCGGACAGCCAAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA
 490 500 510 520 530 540 550
 CTGGAGACAAACCTCGGACAGCCAAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA
 580 590 600 610 620 630 640
 GAAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA
 560 570 580 590 600 610 620
 GAAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA
 650 660 670 680 690 700 710 720
 ATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT
 630 640 650 660 670 680 690
 ATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT
 730 740 750 760 770 780 790
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 700 710 720 730 740 750 760
 TTGATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAAC
 800 810 820 830 840 850 860
 CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC
 770 780 790 800 810 820 830 840
 CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC
 870 880 890 900 910 920 930
 ATTGGAGCTGTGGTATTTGTGGTCAATCCTTGTGTCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAG
 850 860 870 880 890 900 910
 ATTGGAGCTGTGGTATTTGTGGTCAATCCTTGTGTCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAG
 940 950 960 970 980 X
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
 920 930 940 950 960 X 970 980
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCACTGTTGGAGCTAC
 TGCAAATGCTATATTGCACTGTGACCGAG
 990 1000 1010

4. FURM-969863-FIG2.SEQ (1-987)

OCBTF O.cuniculus mRNA for brain tissue factor
 LOCUS OCBTF 1300 bp RNA MAM 31-OCT-1991
 DEFINITION O.cuniculus mRNA for brain tissue factor
 ACCESSION X53521
 KEYWORDS brain tissue factor.
 SOURCE rabbit
 ORGANISM *Oryctolagus cuniculus*
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 Theria; Eutheria; Lagomorpha; Leporidae.
 REFERENCE 1 (bases 1 to 1300)
 AUTHORS Pawashe, A.B.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUL-1990) Pawashe A.B., Yale University, SHM C 115,
 Dept. of Molecular Biophysics & Biochemistry, 333 Cedar Street, POB
 3333, New Haven, CT 06510, USA.
 STANDARD full automatic
 REFERENCE 2 (bases 1 to 1300)
 AUTHORS Pawashe, A.B., Konigsberg, W.K. and Ezekowitz, M.D.
 TITLE Molecular Cloning, Characterization and Expression of cDNA for
 Rabbit Brain Tissue Factor
 JOURNAL Thromb. Haemost. 66, 315-320 (1991)
 STANDARD full automatic
 COMMENT NCBI gi: 1495
 FEATURES
 source 1..1300
 /organism="Oryctolagus cuniculus"
 /strain="new zealand white rabbit"
 exon <1..4
 /number=1
 exon 5..111
 /number=2
 exon 112..311
 /number=3
 exon 712..800

3. FURM-969863-FIG2.SEQ (1-987)

HUMTFPA Human tissue factor mRNA, complete cds, with an Al

LOCUS HUMTFPA 2104 bp ss-mRNA PRI 30-SEP-1988

DEFINITION Human tissue factor mRNA, complete cds, with an Alu repeat in the 3' untranslated region.

ACCESSION M16553

KEYWORDS Alu repeat; plasma membrane glycoprotein; tissue factor.

SOURCE Human placenta, cDNA to mRNA, clones lambda-hTF[3,7,8,12].

ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

REFERENCE 1 (bases 1 to 2104)

AUTHORS Scarpati, E.M., Wen, D., Broze, G.J. Jr., Miletich, J.P., Flandermeyer, R.R., Siegel, N.R. and Sadler, J.E.

TITLE Human tissue factor: cDNA sequence and chromosome localization of the gene

JOURNAL Biochemistry 26, 5234-5238 (1987)

STANDARD full automatic

COMMENT Draft entry and computer-readable sequence for [1] kindly provided by E.M. Scarpati, 04-AUG-1987.

NCBI gi: 339503

FEATURES

mRNA Location/Qualifiers
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sig_peptide 76..174
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/note="tissue factor signal peptide"

mat_peptide 175..960
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/note="tissue factor"

repeat_region 1330..1628
/note="Alu repeat"

CDS 76..963
/gene="F3"
/note="tissue factor precursor; NCBI gi: 339504."
/codon_start=1
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source 1..2104
/organism="Homo sapiens"

BASE COUNT 602 a 437 c 469 g 596 t

ORIGIN SmaI site; chromosome 1.

Initial Score = 958 Optimized Score = 961 Significance = 69.34

Residue Identity = 99% Matches = 961 Mismatches = 2

Gaps = 0 Conservative Substitutions = 0

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      |||
      GGGTGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
      X      10      20      30      40

      80      90      100     110     120     130     140
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC
|||
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC
50      60      70      80      90      100     110     120

      150     160     170     180     190     200     210
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
|||
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
130     140     150     160     170     180     190

      220     230     240     250     260     270     280
GCAGCATATAATTTAACTTGGAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
|||
GCAGCATATAATTTAACTTGGAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
200     210     220     230     240     250     260

      290     300     310     320     330     340     350     360
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACA
|||
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACA
270     280     290     300     310     320     330

      370     380     390     400     410     420     430
GAGTGTGACCTCACCACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCG
|||
GAGTGTGACCTCACCACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCG
340     350     360     370     380     390     400

```

X 10 20 30 40 50 60 70
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 CTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
 X 10 20 30 40 50 60 70
 80 90 100 110 120 130 140
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 GCTCGATCTCGCCGCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC
 80 90 100 110 120 130 140
 150 160 170 180 190 200 210
 GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
 GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
 150 160 170 180 190 200 210
 220 230 240 250 260 270 280
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 GCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCAAT
 220 230 240 250 260 270 280
 290 300 310 320 330 340 350 360
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 CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAATGCTTTTACACAACAGACACA
 290 300 310 320 330 340 350 360
 370 380 390 400 410 420 430
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 GAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCCTACCCG
 370 380 390 400 410 420 430
 440 450 460 470 480 490 500
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 440 450 460 470 480 490 500
 510 520 530 540 550 560 570
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 CTGGAGACAAACCTCGGACAGCCAAATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTA
 510 520 530 540 550 560 570
 580 590 600 610 620 630 640
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 GAAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA
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 650 660 670 680 690 700 710 720
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 ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAACACTAATGAGTTT
 650 660 670 680 690 700 710 720
 730 740 750 760 770 780 790
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 TTGATTGATGTGGATAAAGGAGAAAACACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAAC
 730 740 750 760 770 780 790
 800 810 820 830 840 850 860
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 CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC
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 870 880 890 900 910 920 930
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 ATTGAGCTGTGGTATTTGTGGTCAATCCTTGTGTCATCCTGGCTATATCTCTACACAAGTGTAGAAAG
 870 880 890 900 910 920 930
 940 950 960 970 980 X
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCACTGTTGGAGCTAC
 940 950 960 970 980 990 1000
 TGCAATGCTATATTGCACTGTGACCGAG
 1010 1020 1030

```

640      650      660      670      680      690      700      710      720
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GGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAAC
650      660      670      680      690      700      710      720

710      720      730      740      750      760      770      780
ACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAAACTACTGTTTCAGTGTTCAGCAGTGATTCCTCC
ACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAAACTACTGTTTCAGTGTTCAGCAGTGATTCCTCC
730      740      750      760      770      780      790

790      800      810      820      830      840      850
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CGAACAGTTAACCGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
800      810      820      830      840      850      860

860      870      880      890      900      910      920
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ATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATCTCTACAC
870      880      890      900      910      920      930

930      940      950      960      970      980      X
AAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTCATAA
AAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTCATAAAGGAAGCAC
940      950      960      970      980      990      1000

TGTTGGAGCTACTGCAAATGCTATATTGCACTGTGACCGAG
1010      1020      1030      1040

```

2. FURM-969863-FIG2.SEQ (1-987)

```

HUMTFPC      Human tissue factor gene, complete cds, with a Alu

LOCUS      HUMTFPC      2127 bp ss-mRNA      PRI      15-DEC-1989
DEFINITION      Human tissue factor gene, complete cds, with a Alu repetitive
sequence in the 3' untranslated region.
ACCESSION      M27436
KEYWORDS      Alu repeat; plasma membrane glycoprotein; tissue factor;
transmembrane protein.
SOURCE      Human adult adipose, cDNA to mRNA, clone lambda-TF14.
ORGANISM      Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE      1 (bases 1 to 2127)
AUTHORS      Fisher, K.L., Gorman, C.M., Vehar, G.A., O'Brien, D.P. and Lawn, R.M.
TITLE      Cloning and expression of human tissue factor cDNA
JOURNAL      Thromb. Res. 48, 89-99 (1987)
STANDARD      full automatic
COMMENT      Draft entry and computer-readable copy of sequence [1] kindly
submitted by K.L.Fisher, 30-AUG-1989.
NCBI gi: 339507

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    1354..1651
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  repeat_region
    1652..1662
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    100..987
    /note="tissue factor precursor; NCBI gi: 339508."
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YLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTV
DERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGENYC
FSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHK
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  source
    1..2127
    /organism="Homo sapiens"

BASE COUNT      606 a      450 c      472 g      599 t
ORIGIN

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Initial Score      =      987      Optimized Score      =      987      Significance      = 71.51
Residue Identity    = 100%      Matches                  =      987      Mismatches      =      0
Gaps                =      0      Conservative Substitutions      =      0

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/codon_start=1
/note="tissue factor version 1 signal peptide"
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mat_peptide 208..996
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mat_peptide 214..996
/codon_start=1
/note="tissue factor version 2"
CDS 112..999
/gene="F3"
/note="tissue factor versions 1 and 2 precursor; NCBI gi:
339502."
/codon_start=1
/translation="METPAWPRVPRPETAVARTLLLGNVFAQVAGASGTTNTVAAYNL
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YLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKNVTV
DERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGENYC
FSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILHK
CRKAGVGQSWKENSPLNVS"
source 1..2141
/organism="Homo sapiens"
BASE COUNT 607 a 454 c 478 g 602 t
ORIGIN 87 bp upstream of TaqI site [Cell 50, 129-135 (1987)].

Initial Score = 987 Optimized Score = 987 Significance = 71.51
Residue Identity = 100% Matches = 987 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60
CTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
CGGGCGAACCCCTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
10 X 20 30 40 50 60 70
70 80 90 100 110 120 130
GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCGGGTCCCGCGC
GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCGGGTCCCGCGC
80 90 100 110 120 130 140
140 150 160 170 180 190 200
CCCGAGACCGCCGCTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAAGGTGGCCGGCGCTTCAGGCACT
CCCGAGACCGCCGCTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAAGGTGGCCGGCGCTTCAGGCACT
150 160 170 180 190 200 210
210 220 230 240 250 260 270
ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCC
ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCC
220 230 240 250 260 270 280
280 290 300 310 320 330 340
AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC
AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC
290 300 310 320 330 340 350 360
350 360 370 380 390 400 410 420
ACAACAGACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTC
ACAACAGACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTC
370 380 390 400 410 420 430
430 440 450 460 470 480 490
TTCTCTACCGGCAGGGAATGTGGAGAGACCGGTTCTGCTGGGAGCCTCTGTATGAGAACTCCCCAGAG
TTCTCTACCGGCAGGGAATGTGGAGAGACCGGTTCTGCTGGGAGCCTCTGTATGAGAACTCCCCAGAG
440 450 460 470 480 490 500
500 510 520 530 540 550 560
TTCACACCTTACCTGGAGACAACTCTGGACAGCCAACAATTGAGAGTTTGAACAGGTGGGAACAAAAGTG
TTCACACCTTACCTGGAGACAACTCTGGACAGCCAACAATTGAGAGTTTGAACAGGTGGGAACAAAAGTG
510 520 530 540 550 560 570
570 580 590 600 610 620 630
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
580 590 600 610 620 630 640

4. OCBTF	O.cuniculus mRNA for	1555	361	608	37.61	0
5. RABRTF	Rabbit tissue factor mRNA, co	1753	560	693	39.54	0
**** 30 standard deviations above mean ****						
6. S74147	tissue factor [cattle, adrena	1877	443	759	30.78	0
**** 25 standard deviations above mean ****						
7. HUMTFPB	Human tissue factor gene, com	13865	378	516	25.91	0
**** 23 standard deviations above mean ****						
8. MUSTFA	Mouse tissue factor mRNA, com	1262	344	549	23.36	0
9. MUSTF	Mouse tissue factor (mtf) mRN	1821	343	582	23.29	0
**** 21 standard deviations above mean ****						
10. RRU07619	Rattus norvegicus Sprague-Daw	1683	321	555	21.64	0
11. RNO7619	Rattus norvegicus Sprague-Daw	1683	321	555	21.64	0
**** 11 standard deviations above mean ****						
12. MTPFZ1A	M.thermoformicum complete p	11014	179	435	11.01	0
**** 8 standard deviations above mean ****						
13. PSEPAHAB	P. putida DNA for reductase,	5840	149	419	8.76	0
14. XXMU01	Bacteriophage Mu genome right	1110	142	228	8.24	0
15. CLNCYCA	Clam cyclin A mRNA, complete	2163	139	429	8.01	0
**** 7 standard deviations above mean ****						
16. S55744	T cell receptor variable gamm	446	130	197	7.34	0
17. DATCVG1	O.aries rearranged T-cell rec	604	130	235	7.34	0
18. RNSCIII	Rat mRNA for brain sodium cha	6822	126	407	7.04	0
**** 6 standard deviations above mean ****						
19. PIGRI	Pig ribonuclease inhibitor (R	1256	125	418	6.96	0
20. BGHMGCOA	B.germanica mRNA for HMG-CoA	3433	124	426	6.89	0
21. M24537	Figure 2. Sequence of the spo	3360	122	410	6.74	0
22. BOVCNPA	Bos taurus (clone pCAMPDE-40)	2287	121	261	6.66	0
23. BACPBPE	Bacillus subtilis penicillin-	2362	120	415	6.59	0
24. HUMUT1002	Human STS UT1002.	532	119	217	6.51	0
25. BTCRYB1	Bovine mRNA for beta-crystall	860	119	377	6.51	0
26. HSEF1AL9	Human DNA for elongation fact	1823	119	336	6.51	0
27. DROGGBCS	D.melanogaster (clones T-beta	4590	119	416	6.51	0
28. GOTGLDBE	Goat beta globin locus activa	10194	119	421	6.51	0
29. HSCOMT1	H.sapiens catechol O-methyltr	1844	116	419	6.29	0
30. AA2LEFT	adeno-associated virus 2 left	2116	116	284	6.29	0
31. MFAPDA4A	M.fascicularis gene for apoli	2858	116	425	6.29	0
32. AA2CG	Adeno-associated virus 2, com	4675	116	425	6.29	0
33. PFPFF248	P.falciplarum DNA for erythro	509	115	203	6.22	0
34. HSARYLA	Human DNA for arylsulphatase	3637	115	399	6.22	0
35. BACMSQB	B.thuringiensis insecticidal	3753	115	422	6.22	0
36. HUMFGFAA	Human fibroblast growth facto	3901	115	418	6.22	0
37. MACP53A	Rhesus monkey p53 mRNA sequen	2184	114	416	6.14	0
38. XLAEIIIM	X.laevis AE-III mRNA for pept	3618	114	427	6.14	0
39. S67111	{variable DNA region EhVR1} [1669	113	392	6.07	0
40. HSDAO	H.sapiens diamine oxidase gen	9903	113	417	6.07	0

1. FURM-969863-FIG2.SEQ (1-987)

HUMTFP Human placental tissue factor (two forms) mRNA, co

LOCUS HUMTFP 2141 bp ss-mRNA PRI 15-JUN-1988

DEFINITION Human placental tissue factor (two forms) mRNA, complete cds.

ACCESSION J02931 J02681

KEYWORDS membrane-bound glycoprotein; procoagulant protein; tissue factor.

SOURCE Human placenta, cDNA to mRNA, clones lambda-[10.3 and 10.4] [2]; fibroblast cell line WI38, cDNA to mRNA, library of J.Sorge, clones lambda-CTF12.3,4,5,22,23].

ORGANISM Homo sapiens

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

REFERENCE 1 (bases 79 to 1061)

AUTHORS Morrissey,J.H., Fakhrai,H. and Edgington,T.S.

TITLE Molecular cloning of the cDNA for tissue factor, the cellular receptor for the initiation of the coagulation protease cascade

JOURNAL Cell 50, 129-135 (1987)

STANDARD full automatic

REFERENCE 2 (bases 1 to 2141)

AUTHORS Spicer,E.K., Horton,R., Bloem,L.J., Bach,R., Williams,K.R., Guha,A., Kraus,J., Neemerson,Y. and Konigsberg,W.H.

TITLE Isolation of cDNA clones coding for human tissue factor: Primary structure of the protein and cDNA

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152 (1987)

STANDARD full automatic

COMMENT Draft entry and computer-readable sequence for [2] kindly provided by E.K.Spicer, 03-JUN-1987; and for [1] by J.H.Morrissey, 11-MAY-1987.

Two forms of tissue factor (light and heavy) are thought to be produced by differential cleavage at the 3' end of the signal peptide. The two forms of tissue factor are two amino acids different in length at the amino terminal of the mature protein and are otherwise identical.

A potential polyadenylation signal is located at positions 2119-2124.

NCBI gi: 339501

FEATURES Location/Qualifiers